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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptcdatta/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdatta/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdatta/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdatta/2/iaa/BTUS_COMB.pep:*
6: /cgn2_6/ptcdata/2/iaa/backfIles1.pep:*
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US-08-812-871-3

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US-09-299-843A-44

US-09-170-496D-182

US-08-118-270-3

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ALIGNMENTS

; CLONE: : Patent No. 6063596 IELEX: INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS: LENGTH: 358 amino acids GENERAL INFORMATION: FILING DATE: ATTORNEY AGENT INFORMATION: NAME: Billings, Lucy J. NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-0 TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555 TOPOLOGY: linea. IMMEDIATE SOURCE: PROSTUTO9 ZIP: 94304 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatibl OPERATING SYSTEM: DOS APPLICANT: La1, Landman, Olga APPLICANT: Bandman, Olga APPLICANT: Hillman, Jennifer L. COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FASTSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/988,876 FILING DATE: Herewith CLASSIFICATION: PRIOR APPLICATION NUMBER: APPLICANT: Hillman, Jennifer L. APPLICANT: Yue, Henry TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED TITLE OF INVENTION: WITH IMMUNE RESPONSE NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS: STREET: 3174 Port CITY: Palo Alto STATE: CA COUNTRY: USA STRANDEDNESS: TYPE: TELEFAX: 650-845-4166 ADDRESSEE: amino acid Application US/08988876 E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive single PF-0441 US

Local

Similarity

Length 358;

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CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PERL Program
SEQ ID NO 22
LENGTH: 358
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Faris, Mary
APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No.
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                                                                                                                                                                                                                                                                    Score 1846; DB 4;
Pred. No. 3.8e-138;
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Pred. No. 3.8e-138;
2; Mismatches 3;
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Patent No.
                                                                                                                                                              Matches
                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0441
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/988,876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: C
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TOPOLOGY: li
                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: H
CLASSIFICATION:
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104 FGPWYFKFILCRYTSVLFYANNYTSIVFLGLISIDRYLKVVKPFGDSRMYSITFTKVLSV 163
                                                                                                                                                             147;
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                                           LGPWQLNVFVCRVSAVLFYVNMYVSIVFFGLISFDRYYKIVKPLWTSFIQSVSYSKLLSV
                                                                                                    IIPVLYCMVFIAGILLNGVSGWIFFYVPSSKSFIIYLKNIVIADFVMSLTFPFKILGDSG
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3174 Porter Drive
                                                                                                                                                                                                                                                                                                                    338 amino acids
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Hillman, Jennifer L.
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                                                                                                                                                          64,
                                                                                                                                                                       Score 768.5; DB 3
Pred. No. 2.9e-53;
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; SOFTWARE: FastSEQ for W:
; SEQ ID NO 2
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-303-524A-2
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US-09-303-524A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT PELLIATION NUMBER: US/09/303,524A
CURRENT FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/083,957
PRIOR PILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 2
SOPTWARE: FASTSEQ for Windows Version 3.0
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APPLICANT: ARNOLD, ANNE ROMANIC
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN THE HUMAN KIAA0001
TITLE OF INVENTION: RECEPTOR AND LIGANDS THEREOF
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5, 6238873
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                                         RIKRGNTTL
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SARAU, HENRY M.
FOLEY, JIM
                                                                                SVRRSEVRI 351
                                                                                                                        HYSCOSKEILRYMKEFTLLLSAANVCLDPIIYFFLCOPFREILCKKLHIPLKAONDLDIS
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Best Local Similarity 48.2%;
Matches 146; Conservative 63
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MEDIUM TYPE: FLOPPY DISK
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PATENTIN RELEASE #1.0, VERSION #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILLING DATE: 06-UUN-1995
CLASSIFICATION: 435
CCLASSIFICATION: 435
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APPLICANT: LI, YI
APPLICANT: CAO, L
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 325 amino acids
                                                                                                                                                                                             164 CVWVIMAVLSLPNIILTNGQPTEDNIHDCSKLKSPLGVKWHTAVTYVNSCLFVAVLVILI 223
263 HYSCQSKEILRYMKEFTILLISAANVCLDPIIYFFLCQPFREILCKKLHIPLKAQNDLDIS
                                       283 LLDESAQKILYYCKEITLFLSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTRSESIRSLQ 342
                                                                                                                                                                                                                                                                            104 FGPWYFKFILCRYTSVLFYANMYTSIVFLGLISIDRYLKVVKPFGDSRMYSITFTKVLSV 163
                                                                                                                                                                                                                                                                                                                                                        44 VLPVLYLIIFVASILLNGLAVWIFFHIRNKTSFIFYLKNIVVADLIMTLTFPFRIVHDAG 103
                                                                                                                                                                                                                                                    83 LGPWQLNVFVCRVSAVLFYVNMYVSIVFFGLISFDRYYKIVKPLWTSFIQSVSYSKLLSV 142
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                                                                                                                   GCYIAISRYIHKSS-RQFISQSSRKRKHNQSIRVVVAVFFTCFLPYHLCRIPFTFSHLDR 282
                                                                                                                                                                 IVWMLMLLLAVPNIILTNOSVREVTQIKCIELKSELGRKWHKASNYIFVAIFWIVFLLLI
                                                                                                                                                                                                                                                                                                                                     IIPVLYCMVFIAGILLNGVSGWIFFYVPSSKSFIIYLKNIVIADFVMSLTFPFKILGDSG
                                                                                  VFYTAITKKIFKSHLKSSRNSTSVKKKSSRNIFSIVFVFFVCFVPYHIARIPYTKSQTEA
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CAO, LIANG
NI, JIAN
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BULT, CAROL J
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; Pred. No. 8.4e-53;
63; Mismatches 93;
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Indels Length 325;

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US-08-467-947A-29
                                                                                                                                                                                                                                                     Best Local Similarity Matches 146; Conserv
                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: not
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
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APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Coupled Receptor GPR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: STEFFE, ERIC F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: WASHINGTON
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                                                                                164 CVWVIWAVISLPNIILTNGQPTEDNIHDCSKLKSPLGVKWHTAVTYVNSCLFVAVLVILI 223
                                                                                                                                                        104
                                                                                                                        83
                                                                                                                                                                                       23
                                                                                                                                                                                                                 44 VLPVLYLIIFVASILLNGLAVWIFFHIRNKTSFIFYLKNIVVADLIMTLTFPFRIVHDAG
GCYIAISRYIHKSS-RQFISQSSRKKKHNQSIRVVVAVFFTCFLPYHLCRIPFTFSHLDR 282
                                                                                                                    LGPWQLNVFVCRVSAVLFYVNMYVSIVFFGLISFDRYYKIVKPLWTSFIQSVSYSKLLSV
                                                                                                                                                   FGPWYFKFILCRYTSVLFYANMYTSIVFLGLISIDRYLKVVKPFGDSRMYSITFTKVLSV 163
                                                   IVWMLMLLLAVPNÍ ILTNOSVREVTOIKCIELKSELGRKWHKASNYIFVAIFWIVFLLLI
                                                                                                                                                                                  IIPVLYCMVFIAGILLNGVSGWIFFYVPSSKSFIIYLKNIVIADFVMSLTFPFKILGDSG
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1100 NEW YORK AVE.,
                                                                                                                                                                                                                                                                                                                                                                                                 325 amino acids
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CAO, LIANG
NI, JIAN
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BULT, CAROL J.
SUTTON III, GRANGER G.
ROSEN, CRAIG A.
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not relevant
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48.2%; Pred
48.63;
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                                                                                                                                                                                                                                                 Score 762.5; DB 3;
Pred. No. 8.4e-53;
3; Mismatches 93;
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                                                                                                                                                                                                                                                                                  Length 325;
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ADDRESSEE:

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; ORGANISM: genomic
US-08-852-824-2
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US-08-852-824-2
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                                                                                                                                                                      GENERAL INFORMATION:
GENERAL SATHE, GANESH
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TITLE OF INVENTION: Human G-Protein Coupled Receptors
FILE REFERENCE: 1488.1220000
CURRENT APPLICATION NUMBER: US/08/852,824C
CURRENT FILING DATE: 1997-05-04
NUMBER OF SEQ ID NOS: 18
APPLICANT: SATHE, GANESH
APPLICANT: HALSEY, WENDY
APPLICANT: HOUR, ALISON
APPLICANT: CHAMBERS, JON
APPLICANT: SZEKERES, PHILIP
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS OF THE HNEAAB1 REC
NUMBER OF SEQUENCES: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 NRSDGPGKNTTL---HNEFDTIVLPVLYLIIFVASILLNGLAVWIFFHIRNKTSFIFYLK 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 NITSAPG-NTSICTRDYKITOVLFPLLYTVLFFVGLITNGLAMRIFFQIRSKSNFIIFLK 64
                                                                                                                                                                                                                                                                                                                                                          SFRNSLI -- SMLKCPNSATSLSQDNRKKE 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VFFTCFLPYHLCRIPFTFSHLDRLLDESAQKILYYCKEITLFLSACNVCLDPIIYFFMCR
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RESULT 9
US-09-558-740-2
; Sequence 2, Application US/09558740
; Patent No. 6358695
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                            GENERAL INFORMATION:
APPLICANT: SATHE, GAN
APPLICANT: HALSEY, V
APPLICANT: MUIR, ALI
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Best Local (
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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APPLICATION NUMBER: 08/9:
FILING DATE: 23-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FASTSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: P.O. CITY: Valley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                              317 MCRSFSRRL 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 36.8%; Score 690.5; DB 3; Similarity 41.1%; Pred. No. 4.1e-47;
                                                                                                                                                                                                                                              VVAVEFVCFAPFHFARVFYTHSQTNNKTDCRLQNQLFIAKETTLFLAATNICMDFLIYIF 298
                                                                                                                                                                                                                                                                          VVAVFFTCFLPYHLCRIPFTFSHLDRLLDESAQKILYYCKEITLFLSACNVCLDPIIYFF 316
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HALSEY, WENDY
MUIR, ALISON
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CHAMBERS, JON
SZEKERES, PHILIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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RESULT 10
US-08-812-871-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOPTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08812871 Patent No. 5955303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 127; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl
APPLICANT: Muzong Cheng
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING DATE: Filed Herewith
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
PRIOR APPLICATION DATA:
                                                                                                                                                                                                    COUNTRY: U
                                                                                                                                                                                                                                             STREET: 3174 POI
CITY: Palo Alto
STATE: CA
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41.1%; Pred. No. 4.1e-47;
tive 66; Mismatches 97; Indels 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
                                                                                                       APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
CORRESSPONDENCE ADDRESS:
                                                                                                                                                                                                                                                 APPLICANT:
COMPUTER READABLE FORM
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LIBRARY: MMLR3
CLONE: 568987
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LENGTH: 333 amino acids
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              COUNTRY: U
ZIP: 20005
                                             ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVE., NW, SUITE 600 CITY: WASHINGTON STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
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                               USA
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NI, JIAN
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                                                                                                                                                             Human
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                            APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPY DAISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                      NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                      TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein TITLE OF INVENTION: Coupled Receptor GPR1
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LENGTH: 293 amino acids
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                      CITY: WASHINGTON
                                                                                                                                        STREET:
                                                                                      COUNTRY:
                                                                                                                                                        ADDRESSEE:
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REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
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es 85; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                  No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 LKWHOMVNNICOFIFWTVFILMLVFYVVIAK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 LKVVKPFGDSRMYSITFTKVLSVCVWVIMAVLSLPNIILTNGQPTEDNIHDCSKLKSPLG
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                                                                                                                                    E: STERNE, KESSLER,
1100 NEW YORK AVE.,
                                                                                                                                                                                                                                                                                                             LI, YI
CAO, LIAN
NI, JIAN
                                                                                      USA
                                                                                                                                                                                                                                        GENTZ, REINER
BULT, CAROL J.
SUTTON III, GRANGER G.
ROSEN, CRAIG A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                              LIANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.9%; Score 466; DB 2;
40.3%; Pred. No. 1.8e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1488.1140003/EKS/KLM
                                                                                                                                      GOLDSTEIN & FOX P.L.L.C
NW, SUITE 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 293;
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PC-DOS/MS-DOS

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US-08-702-344-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 28, App.
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/I
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
               SOPTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                           APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                   STREET: 87 Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                COUNTRY: U.S.A.
                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 VKWHTAVTYVNSCLFVAVLVILIGCYIAISR 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 KNIVVADLIMTLTFPFRIVHDAGFGPWYFKFILCRYTSVLFYANMYTSIVFLGLISIDRY 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 NTTLHNEF-----DT----IVLPVLYLIIFVASILLNGLAVWIFFHIRNKTSFIFYL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 NTTVMQGFNRSKRCPKDTRIVQLVFPALYTVVFLTGILLNTLALWVFVHIPSSSTFIIYL
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                                                                                                                                                                 Massachusetts
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                                                                                                                                                                                              87 CambridgePark Drive
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LaVallie, Edward
                                                                                                                                                                                                                                                                                                                                                                           Racie, Lisa
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                                                                                                                                                                                                                         Genetics Institute, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.9%; Score 466; DB 3;
40.3%; Pred. No. 1.8e-29;
tive 47; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT/US95/04079
US/08/702,344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6063596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity Matches 83; Conserv
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INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTMARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED REC
TITLE OF INVENTION: WITH IMMUNE RESPONSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS: Incyte Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                    APPLICATION NUMBER: FILING DATE: Herewi
                                       CLASSIFICATION:
                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                       ZIP: 94304
                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 YIAISRYIHKSSRQFISQSSRKRKHNQSIRVVVAVFFTCPLPYHLCRIPFTFSHLDRLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 MVLLIMVPNMMIPIKDIKEKSNVGCMEFKKEFGRNWHLLTNFICVAIFLNFSAIILISNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 YFKFILCRYTSVLFYANMYTSIVFLGLISIDRYLKVVKPFGDSRMYSITFTKVLSVCVWV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 KLKIFHCQVTACLIYINMYLSIIFLAFVSIDRCLQLTHSCKIYRIQEPGFAKMISTVVWL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 FYLVFLVGIIGSCFÁTWAFIQKNTNHRCVSIÝLINLLTÁDFLLŤLALÞVKÍVVDLGVAÞW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 YLIIFVASILLINGLAVWIFFHIR-NKTSFIFYLKNIVVADLIMTLTFPFRIVHDAGFGPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSTRISLFKAKEATLLLAVSNLCFDPILYYHLSKAFRSKV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMAVLSLPNIILTNGQPTEDNIHDCSKLKSPLGVKWHTAVTYVNSCLFV--AVLVILIGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08988876
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(617) 876-5851
(617) B76-5851
                                                                                                                                                                                                                                                                                   3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319 amino acids
                                                                                                                                                                                                                                                                                                                                                                                        Bandman, Orya
Hillman, Jennifer L.
                                                                                                                                                                                                                            USA
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                                                      Herewith
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29.6%; Pred. No. 7.4e-26;
Live 64; Mismatches 126
                                                                                                                                                                                                                                                                                                                                                                             G PROTEIN COUPLED RECEPTORS ASSOCIATED
                                                                          US/08/988,876
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ATTORNEY/AGENT INFORMATION:

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US-09-585-876-2
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                                                                             ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-585-876-2
                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09585876 Patent No. 6586205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 96;
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Best Local Similarity
Query Match
Best Local Similarity
Matches 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                               APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Silos-Santiago, Immaculada
TITLE OF INVENTION: 43239, A No. 6586205el GPCR-Like Molecule and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 5800-88
CURRENT APPLICATION NUMBER: US/09/585,876
CURRENT APPLICATION NUMBER: US/09/585,876
CURRENT FILING DATE: 2000-06-01
EARLIER APPLICATION NUMBER: 60/182,061
EARLIER FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 342 amino acid
                                                                                                                                       LENGTH: 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0441 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-055
TELEPAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
LIBRARY: GenBank
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSKLKSPLGVKWHTAVTYVNSCL---FVAVLVILIGCYIAISRYIHKSSRQFISQSSR--
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  19.9%; Score 372; DB 4; Length 346; ilarity 28.4%; Pred. No. 5.3e-22; Conservative 68; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                               135 VRFLAMVHPFRLLHVTSIRSAWILCGIWILIMASSI--MILDSGSEQNGSVTSCLELNL 192
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  304
                                                 313 IYFFMCRSFSRRLFKKSNIR-----TRSESIRSLQSVRRSEVRI 351
                                                                                                  248 TIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALV----ITLVLAAANACFNPL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 EMEPNGTFSNNNSRNCTIEN-FKREFPFIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVN 74
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LYYFAGENFKDRL--KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346
                                                                                                                                              VVV---AVEPTCFLPYHLCRIPFTFSHLDRLLDESAQKILYYCKEITLFLSACNVCLDPI 312
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Search completed: June 1, 2004, 15:19:51 Job time : 24 secs

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

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Match Length
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    US-09-826-508-10
US-09-741-783-1
US-10-15-844-1
US-10-225-567A-418
US-10-225-567A-18
US-10-295-027-364
US-10-295-027-125-56
US-10-692-605-18
US-10-692-605-18
US-09-919-172-22
US-09-919-172-28
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Sequence 10, Appli
Sequence 1, Appli
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Sequence 418, App
Sequence 1255, App
Sequence 1255, App
Sequence 135, Appl
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Sequence 22, Appli
Sequence 86, Appli
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Sequence 77, Appli
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US-09-769-159-2	US-10-692-605-8	US-10-308-968-2	US-10-352-684A-34	US-10-225-567A-514	US-10-243-106-2	US-09-957-187-2	-125-	US-09-745-842-4	US-10-417-820A-34	US-10-393-807-32	US-10-272-983-32	US-10-333-844-2	US-10-225-567A-643	US-10-343-650A-26	US-09-876-252-34	US-09-875-076-32	US-09-745-842-6	US-09-964-008-1	US-09-780-576-2	US-09-827-937A-2	US-09-835-922-2	US-09-745-842-2	US-10-189-576-2	US-10-433-146-2	US-09-826-508-20	US-10-024-494-29	US-10-352-684A-42	US-10-225-567A-213	US-10-121-101B-10
Sequence 2, Appli	8,	2, 1	34,	Sequence 514, App	2,	'n	N	4.	34	32,	32	'n	643	26,	34 4	32	e 6,	Sequence 1, Appli	Sequence 2, Appli	٧,	2,	'n	'n	e 2,	20,	29,	e 42,	Sequence 213, App	Sequence 10, Appl

ALIGNMENTS

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US-09-826-508-10
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CURRENT FILING DATE: 2001-04-05
NUMBER OF SEO ID NOS: 40
SOPTWARE: FASTSEQ for Windows Version 3.0
SEO ID NO 10
LENGTH: 358
TYPE: PAT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/09826508
Patent No. US20010025099A1
GENERAL INFORMATION:
APPLICANT: Nabil Elshourbagy
APPLICANT: Lisa Vawter
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Best Local (
                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                         'Match 100.0%; Score 1874; DB 9; Length 3
Local Similarity 100.0%; Pred. No. 6.3e-162;
Les 358; Conservative 0; Mismatches 0; Indels
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NGQPTEDNIHDCSKLKSPLGVKMHTAVTYVNSCLFVAVLVILIGCYIAISRYIHKSSRQF
                                                                                      FYANMYTSIVFLGLISIDRYLKVVKPFGDSRMYSITFTKVLSVCVWVIMAVLSLPNIILT 180
                                                                                                                                               GLAVWIFFHIRNKTSFIFYLKNIVVADLIMTLTFPFRIVHDAGFGPWYFKFILCRYTSVL
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RESULT 3
US-10-165-844-1
US-10-165-844-1
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Best Local S
Matches 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/464,685
PRIOR TILING DATE: 1999-12-16
PRIOR PILICATION NUMBER: 09/324,465
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: 09/088,857
PRIOR FILING DATE: 1998-06-02
NUMBER: 0F SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Glucksmann, Maria A.
APPLICANT: Hodge, Martin R
APPLICANT: Hunter, John J.
APPLICANT: Rudolph-Owen, Laura
APPLICANT: Rudolph-Owen, Laura
APPLICANT: Weich, Nadine S.
TITLE OF INVENTION: 2871 RECEPTOR, A NOVEL G-PROTEIN COUPLED RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 35800/207283
CURRENT APPLICATION NUMBER: US/09/741,783
CURRENT FILING DATE: 2000-12-18
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                      NGQPTEDNIHDCSKLKSPLGVKWHTAVTYVNSCLFVAVLVILIGCYIAISRYIHKSSRQF
                                                                                                      FLSACNVCLDPITYFFMCRSFSRRLFKKSNIRTRSESIRSLQSVRRSEVRIYYDYTDV 358
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GENERAL

RESULT 4 US-10-225-567A-418

Sequence 418, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.

APPLICANT:

Brown, Joseph P. Burmer, Glenna C. Roush, Christine

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US-10-165-844-1
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CUERENT APPLICATION NUMBER: US/10/165,844
CUERENT FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 09/088,857
PRIOR PELING DATE: 1998-06-02
PRIOR PELING DATE: 1999-06-02
PRIOR PELING DATE: 1999-12-16
PRIOR PELING DATE: 1999-12-16
PRIOR PELING DATE: 1999-12-18
PRIOR PELING DATE: 1999-12-18
PRIOR PELING DATE: 2000-12-18
PRIOR PELING DATE: 2000-12-18
PRIOR PELING DATE: 1999-12-16
PRIOR PELING DATE: 1999-00-26
PRIOR PELING DATE: 1999-00-26
PRIOR APPLICATION NUMBER: US 09/145,745
PRIOR PELING DATE: 1999-00-26
PRIOR APPLICATION NUMBER: US 09/340,880
PRIOR PELING DATE: 1999-06-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Rudolph-Owen, Laura
APPLICANT: Weich, Nadine S.
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: Novel Nucleic Acid Sequences
TITLE OF INVENTION: G-Protein Coupled Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Glucksmann, Maria Alexandra APPLICANT: Hodge, Martin_R.
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                          FLSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTRSESIRSLQSVRRSEVRIYYDYTDV
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                                                                                      ISQSSRKRKHNQSIRVVVAVFFTCFLPYHLCRIPFTFSHLDRLLDESAQKILYYCKEITL
                                                                                                                   ISQSSRKRKHNQSIRVVVAVFFTCFLPYHLCRIPFTFSHLDRLLDESAQKILYYCKEITL
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Pred. No. 6.3e-162;
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FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 418
LENGTH: 358
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US-10-295-027-364
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CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR PILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-21
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APPLICANT: Aziz, Natash
APPLICANT: Ginsberg, Wei
APPLICANT: Gish, Kurt C
APPLICANT: Glynne, Rich
APPLICANT: Hevezi, Pete;
APPLICANT: Mack, David i
APPLICANT: Mack, David i
APPLICANT: Mack, David i
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                                                                                                                                                                                                                                                                                                                  APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
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Local Similarity 100.0%; Pred. No. 6.3e-162;
hes 358; Conservative 0; Mismatches 0; Indels
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Hevezi, Peter A.
Mack, David H.
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PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR PILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR PILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR FILING DATE: 2002-02-13
PRIOR PILING DATE: 2002-02-06
PRIOR PILING DATE: 2002-02-06
PRIOR PILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR PILING DATE: 2002-02-13
PRIOR PILING DATE: 2002-02-13
Remaining Prior Application data removed - See
NUMBER OF SEQ ID NOS: 1386
SOCTWARE: Patentin Ver. 2.1
SEQ ID NO 364
LENGTH: 358
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Similarity 100.0%; F
58; Conservative 0;
                     FLSACNVCLDFIIYFFMCRSFSRRLFKKKSNIRTRSESIRSLQSVRRSEVRIYYDYTDV
                                                                                         ISQSSRKRKHNQSIRVVVAVFFTCFLFYHLCRIFFTFSHLDRLLDESAQKILYYCKEITL
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FLSACNVCLDPITYFFMCRSFSRRLFKKSNIRTRSESIRSLQSVRRSEVRIYYDYTDV
                                                                                                                                               NGQPTEDNIHDCSKLKSPLGVKWHTAVTYVNSCLFVAVLVILIGCYIAISRYIHKSSRQF
                                                                       ISQSSRKRKHNQSIRVVVAVFFTCFLPYHLCRIPFTFSHLDRLLDESAQKILYYCKEITL
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Pred. No. 6.3e-162;
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WS-10-295-027-1255
US-10-295-027-1255
Sequence 1255, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Afar, Daniel
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Matson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
APPLICANT: Eos Biotechnology, Inc.
APPLICANT: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Screening for Modulators of CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/350,334
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APPLICANT: Mack, David H.
APPLICANT: Aziz, Natasha
APPLICANT: Bos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
TITLE OF INVENTION: Cancer
FILLE REFERENCE: 018501-002330US
CURRENT APPLICATION NUMBER: US/10/188,832
CURRENT APPLICATION NUMBER: US 60/302,814
PRIOR APPLICATION NUMBER: US 60/302,814
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: US 60/310,099
PRIOR APPLICATION NUMBER: US 60/310,099
PRIOR APPLICATION NUMBER: US 60/310,099
PRIOR APPLICATION NUMBER: US 60/343,705
PRIOR FILING DATE: 2001-11-08
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US-10-188-832-135
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PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR PILING DATE: 2001-12-14
PRIOR PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-10
PRIOR PILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR PRILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR APPLICATION DATE: 2002-02-13
Remaining Prior Application data removed - SEC ID NOS: 1386
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-10-295-027-1255
                                                                                                                                                                                                                                                                                                                           Sequence 135, Applic Publication No. US20 GENERAL INFORMATION:
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Best Local Similarity
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TYPE: PRT
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o. US20040076955A1
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PRIOR APPLICATION NUMBER: US 09/429,55.

PRIOR APPLICATION UNBER: US 09/429,55.

PRIOR APPLICATION NUMBER: US 09/429,55.

PRIOR APPLICATION NUMBER: US 09/429,676

PRIOR APPLICATION NUMBER: US 09/429,676

PRIOR APPLICATION NUMBER: US 09/429,695

PRIOR FILING DATE: 1999-10-28

PRIOR APPLICATION NUMBER: US 09/428,114

PRIOR APPLICATION NUMBER: US 09/428,114

PRIOR APPLICATION NUMBER: US 09/428,020

TOR APPLICATION NUMBER: US 09/428,020
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/698,419
PRIOR FILING DATE: 2000-10-27
PRIOR PELICATION NUMBER: US 09/481,794
PRIOR PELICATION NUMBER: US 09/481,794
PRIOR APPLICATION NUMBER: US 09/454,399
PRIOR PILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: US 09/429,517
PRIOR APPLICATION NUMBER: US 09/429,555
PRIOR APPLICATION NUMBER: US 09/429,555
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US-10-692-605-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18, Application US/10692605
Publication No. US20040091928A1
GENERAL INFORMATION:
APPLICANT: Vogeli, Gabriel
APPLICANT: Wood, Linda S.
APPLICANT: Wood, Linda S.
APPLICANT: Merchant, Kalpana
TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTORS EXPRESSED IN BRAIN
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Best Local Sim
Matches 358;
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SEQ ID NO 135
LENGTH: 358
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/692,605
CURRENT FILING DATE: 2003-10-24
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PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/372,246
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 207
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GENERAL INFORMATION:

APPLICANT: Faris, Mary
APPLICANT: TURNEr, Christopher M.
APPLICANT: TURNEr, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT APPLICATION NUMBER: 60/222,469
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR PILLING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PERL Program
SEQ ID NO 22
LENGTH: 358
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-919-172-22
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Patent No. US20020119463A1
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Best Local &
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                                                                                                                                                                        FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020119463A1 1650519CD1
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nes 357; Conserv
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                                                                                                                           Similarity 98.6%;
 FLSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTRSESIRSLQSVRRSEVRIYYDYTDV 358
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                                                        MGFNLTLAKLPNNELHGQESHNSGNRSDGPGKNTTLHNEFDTIVLPVLYLIIFVASILLN
                                                                                    MGFNLTLAKL PNNELHGQESHNSGNRSDGPGKNTTLHNEFDTIVLPVLYLII FVASILLN
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99.7%;
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Pred. No. 2.7e-161;
0; Mismatches 1;
                                                                                                                           Score 1846; DB 9;
Pred. No. 2.2e-159;
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                                                                                                                 Mismatches
                                                                                                                                         Length 358;
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RESULT 11
US-10-121-101B-1
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PATENT NO. US20020156263A1

GENERAL INFORMATION:
APPLICANT: Chen, Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CAI
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL PROGram
SEQ ID NO 86
LENGTH: 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 1650519CD1
US-09-974-298-86
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Best Local Similarity 98.6%;
Matches 353; Conservative
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FLSACNVCLDFIIYFFMCRSFSRRLFKKSNIRTRSESIRSLQSVRRSEVRIYYDYTDV 358
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                                                                             ISOSSRKRKHNOSIRVVVAVYFTCFLPYHLCRMPSTFSHLDRLLDESAQKILYYCKEITL
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Pred. No. 2.2e-159;
2; Mismatches 3;
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Application US/10121101B

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RESULT 12
US-10-264-237-2659
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                                                                                                                                                                                     Sequence 2659, Application US/10264237
Publication No. US20040009491A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
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SEQ ID NO 1
LENGTH: 358
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Best Local
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OTHER INFORMATION: Incyte ID No.
-10-121-101B-1
                                                                     FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
                   PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
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CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 09/470,252
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: 08/988,876
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TITLE OF INVENTION: GPCR Diferentially Expressed
FILE REFERENCE: PV-0004 CIP
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NUMBER OF SEQ ID NOS: 11
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ORGANISM: Homo sapiens
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ID NO 2659
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Krasnow, Randi
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98.6%;
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Pred. No. 2.2e-159;
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; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo ;
US-09-919-497-77
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US-09-919-497-77
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                                                          SOFTWARE: P
SEQ ID NO 77
                                                                                                                                                                                                      Patent No. US20020106662A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                   Sequence 77,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 170;
                                                                                                APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION
FILE REFERENCE: BO801/725
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
                                                                                       NUMBER OF SEQ ID NOS: 100
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OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa
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NAME/KEY: MISC_FEATURE
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Pred. No. 9.4e-73;
0; Mismatches 2
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SEQ ID NO 13
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-745-842-13
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; OTHER INFORMATION: UDP-glucose receptor; KIAA0001 gene product
US-09-745-842-13
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APPLICANT: Hollopeter, Gunter
APPLICANT: COR Therapeutics, Inc.
TITLE OF INVENTION: P2Y12 Receptor
FILE REFERENCE: 44481-5053-US
CURRENT APPLICATION NUMBER: US/09/745,842
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: US 60/171,622
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 21
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 21
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                                                                                                                                    84 LGPWQLNVFVCRVSAVLFYVNMYVSIVFFGLISFDRYYKIVKPLWTSFIQSVSYSKLLSV
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GCYIAISRYIHKSS-RQFISQSSRKKKHNQSIRVVVAVFFTCFLPYHLCRIFFTFSHLDR
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Ramakrishnan-DuBridge, Vanitha
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64; Mismatches 97;
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US-10-433-146-1
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LENGTH: 338
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Best Local Similarity
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CURRENT FILLING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: PCT/US01/45076
PRIOR PILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: U.S. 60/250,727
PRIOR FILLING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lee, Byeong-Chel
TITLE OF INVENTION: METHODS AND PRODUCTS FOR MANIPULATING
TITLE OF INVENTION: HEMATOPOIETIC STEM CELLS
FILE REPERENCE: M00765.70039.US
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324
                                                                                                                                                                                                                                   144 IVWMLMLLLAVPNIILTNQSVREVTQIKCIELKSELGRKWHKASNYIFVAIFWIVFLLLI
                                                                                                                                                                                                                                                          164 CVWVIMAVLSLPNIILTNGQPTEDNIHDCSKLKSPLGVKWHTAVTYVNSCLFVAVLVILI 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147;
                                  343 SVRRSEVRI
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                                                                                                                                                                                                                                                                                                                                        104 FGPWYFKFILCRYTSVLFYANMYTSIVFLGLISIDRYLKVVKPFGDSRMYSITFTKVLSV 163
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                                                                                                                                                                                                                                                                                                                                                                                                                84 LGPWQLNVFVCRVSAVLFYVNMYVSIVFFGLISFDRYYKIVKPLWTSFIQSVSYSKLLSV 143
                                                                                                LLDESAQKILYYCKBITLFLSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTRSESIRSLQ 342
                                                                                                                                                                                      GCYIAISRYIHKSS-RQFISQSSRKRKHNQSIRVVVAVPFTCFLPYHLCRIPFTFSHLDR 282
RIKRGNTTL
                                                                         HYSCQSKEILRYMKEFTLLLSAANVCLDPIIYFFLCQPFREILCKKLHIPLKAQNDLDIS
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ilarity 47.6%;
Conservative 6
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332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 768.5; DB 12; Length 338;
Pred. No. 1.6e-61;
Mismatches 97; Indels 1;
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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ALIGNMENTS

							<u> </u>	_	_
QY 306 NVCLDPIIVFFMCRSFSRRLFKKSNIRTRSESIRSLQSVRRSBVRIYYDYTDV 358	Qy 247 -KRKHNQSIRVVVA\VEFTCELPYHLCRIPETESHLDRLLDESAQKILYYCKEITLELSAC 305 : : : : : : : : : :	QY 192 CSKLKSPLGVKWHTAVTYVNSCLFVAVLVILIGCYIAISRYIHKSSRQFISQSSR 246 :	Qy 139 RYLKUVKPEGDSRMYSITETKVLSVCVMVIMAVLSLPNIILTNGQPTEDNIHD 191	Qy 79 YLKNIVVADLIMTLTFPFRIVHDAGFGPWYFKFILCRYTSVLFYANMYTSIVFLGLISID 138 :: : : : : :	Qy 22 NSGNRSDGPGKNTTLHNEEDTIVLPVLYLLIFVASILLNGLAVWIFFHIRNKTSFIF 78	Query Match 20.0%; Score 375.5; DB 2; Length 342; Best Local Similarity 27.2%; Pred. No. 6.4e-25; Matches 96; Conservative 74; Mismatches 148; Indels 35; Gaps 9;	A;Accession: S13638 A;Accession: S19638 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-342 <hon> A;Residues: 1-342 <hon> A;Cross-references: GB:X56736; NID:g49442; PIDN:CAA40060.1; PID:g49443 A;Cross-references: GB:X56736; NID:g49442; PIDN:CAA40060.1; PID:g49443 A;Note: the species of guinea pig is not identified; in GenBank entry CCPAFREC, release C;Superfamily: ATP receptor P2u</hon></hon>	RESULT 1 \$13638 \$13638 platelet-activating factor receptor - guinea pig platelet-activating factor receptor - guinea pig C.Species: Cavia porcellus (guinea pig) C.Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 08-Oct-1999 C.Accession: \$13638 C.Hoccession: \$13638 R.Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H.; To Nature 349, 342-346, 1991 A.Title: Cloning by functional expression of platelet-activating factor receptor from gu A.Reference number: \$13638; MUID:91101726; PMID:1846231	

RESULT 2
\$43252
\$43252
platelet-activating factor receptor - rat
C;Species: Kattus norvegicus (Norway rat)
C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
S63666
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A; Residues: 1-341 <ISH>
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R,Bito, H.; Honda, Z.; Nakamura, M.; Shimizu, T.
Eur. J. Biochem. 221, 211-218, 1994
A;Title: Cloning, expression and tissue distribution of
A;Reference number: S43252; MUID:94222063; PMID:8168510
A;Accession: S43252
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A;Residues: 1-341 <BIT>
A;Cross-references: GB:U04740; NID:g470384;
C;Superfamily: ATP receptor P2u
                                                                                                                                                                                                                                                                        Cross-references: EMBL:D50872; NID:g1256924; PIDN:BAA09468.1; PID:g1256925; Superfamily: ATP receptor P2u
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                                                                                                                                                                                                                           Similarity
NRYQAVAYPIKTAQATTRKRGISLSLIIWV--SIVATASYFLATDSTNLVPNKDGSGNIT
                                                                  DRYLKVVKPFGDSRMYSITFTKVLSVCVWVIMAVLSLPNIIL----TNGQPTED---NIH 190
                                                                                                  FYLKNIVVADLIMTLTFFFFRIVHDAGFGFWYFKFILCRYTSVLFYANMYTSIVFLGLISI 137
                                                                                                                                                                      HNSGNRSDGPGKNTTLHNEFDTIVLPVLYLIIFVASILLNGLAVWIFFHI---RNKTSFI 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICFVPHHVVQLPWTLAELG--YQTNFHQAINDAHQITLCLLSTNCVLDPVIYCFLTKKFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVTYVNSCLFVAVLVILIGCYIAISRYIHKSSRQFISQSSR----KRKHNQSIRVVVAVFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEFDTIVLPVLYLIIFVASILLNGLAVWIF---FHIRNKTSFIFYLKNIVVADLIMTLTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKRGIT----LSLVIWISIAATASYFLATDSTNVVPKKDGSGNITRCFEHYEPYSVPILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RMYSITFTKVLSVCVWVIMAVLSLPNIIL--TNGQPTED---NIHDCSKLKSPLGVKWHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLWIVYYSNEGDWIVHKFLCNLAGCLFFINTYCSVAFLGVITYNRYQAVAYPIKTAQATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFRIVHDAGFGPWYFKFILCRYTSVLFYANWYTSIVFLGLISIDRYLKVVKPF----GDS
                                                                                                                                                                                                           Conservative
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28.7%;
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                                                                                                                                      67,
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                                                                                                                                                                                                                          Score 356.5;
Pred. No. 2.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 360; DB 2;
Pred. No. 1.4e-23;
                                                                                                                                                                                                          Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 134;
                                                                                                                                                                                                                          2.8e-23;
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A;Molecule type: mRNA
A;Residues: 1-399 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Nystedt, S.; Larsson, A.K.; Aberg, H.; Sundelin, J. J. Biol. Chem. 270, 5950-5955, 1995
A;Title: The mouse proteinase-activated receptor-2 cDNA A;Reference number: 148705; MUID:95197820; PMID:7890726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteinase activated receptor 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: I48705
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R;Nystedt, S.; Lars:
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Matches
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                                                                                                                                                                                                                                                                               131 PLKISYHLHGNNWVYGEALCKVLIGFFYGNMYCSILFMTCLSVQRYWVIVNPMGHPRK-K
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                                                                                                   LPYHLCRIPFTFSHLDRLLDESAQKILYYCKEITLFLSACWVCLDPIIYFFMCRSFSRRL
                                                                                                                                                                                                                                                                                                                                                                           LHNBEDTIVLEVLYLIIFVASILLNGLAVWIF-FHIRNKTSFIFYLKNIVVADLIMTLTF
--RDHAR-NALLCRSVRTVNRMQISL
                                 FKKSNIRTRSESIRSLQSVRRSEVRI 351
                                                                     APSNLLLVVHYF---
                                                                                                                                        NYFLSLAIGVFLFPALLTASAYVLMIKTLRSSAMDEHSEKKRORAIRLIITVLAMYFICF
                                                                                                                                                                      NSCLEVAVLVILIGCYIAISRYI--HKSSRQFISQSSRKRKHNQSIRVVV---AVFFTCF
                                                                                                                                                                                                          ANIAVGVSLAIWLLIFLYTIPLYVMKQTIYIPALNITTCHDVLPEEVLVG-----DMF
                                                                                                                                                                                                                                              ITFTKVLSVCVWVIMAVLSLPNIIL--TNGQPTED--NIHDCSKLKSPLGVKWHTAVTYV
                                                                                                                                                                                                                                                                                                                                                       LTGKLTTVFLPVVYIIVFVIGLPSNGMALWIFLFRTKKKHPAVIYMANLALADLLSVIWF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RCFEHYEPYSVPILVVHVFIAFCFFL-VFFLIFYCNLVI---IHTLLTQPMRQQRKAGVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRALWMVCTVLAVFIICFVPHHVVQLPWTLAELG--YQTNFHQAINDAHQITLCLLSTNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKHNQSIRVVVAVEFTCFLPYHLCRIPFTFSHLDRLLDESAQKILYYCKEITLFLSACNV 307
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             18.6%;
                                                                     -LIKTOROSHVYALYLVALCLSTLNSCIDPFVYYFVSKDF----
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 349; DB 2;
Pred. No. 1.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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and

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RESULT 5
$66679

G protein-coupled receptor - human
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: $68679
R;Stam, N.J.; Klomp, J.; van de Heuvel, M.; Olijve, W.
FEBS Lett: 384, 260-264, 1996
A;Title: Molecular cloning and characterization of a novel orphan receptor
A;Reference number: $68679; MUID:96197801; PMID:8617367
A;Accession: $68679
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-365 <STA>
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(P(2P))

expre

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RESULT 6

S66518

proteinase-activated receptor 2 precursor - human

C;Species: Homo sapiens (man)

C;Date: 28-Oct-1996 #sequence revision 13-Mar-1997 #text_change 17-Nov-2000

C;Accession: S66518; S64709; G02131

R.Nystedt, S.; Emilsson, K.; Larsson, A.K.; Stroembeck, B.; Sundelin, J.

Eur. J. Biochem. 232, 84-89, 1995

A;Title: Molecular cloning and functional expression of the gene encoding the A;Accession: S66518; MUID:96048032; PMID:7556175

A;Accession: S66518

A;Status: preliminary

A;Status: preliminary
                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-137, 'A; (139-397 < BOE)
A; Cross-references: EMBL: U34038; NID: g1041728; PIDN: AAB47871.1; PID: g1041729
A; Note: the authors translated the codon GTC for residue 68 as Ile and AAC fc
A; Note, M.L.; Coughlin, S.R.
submitted to the EMBL Data Library, September 1995
A; Reference number: H00822
A; Accession: G02131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-397 < NYS>
A; Residues: 1-397 < NYS>
A; Residues: 1-397 < NYS>
A; Cross-references: EMBL: Z49993; NID: 91008084; PIDN: CAA90290.1; PID: 91008085
R; Boehn, S.K.; Kong, W.; Broemme, D.; Smeekens, S.P.; Anderson, D.C.; Connol.
Blochem. J. 314, 1009-1016, 1996
Blochem. J. 314, 1009-1016, 1996
A; Title: Molecular cloning, expression and potential functions of the human pareference number: S64709; MUID: 96177879; PMID: 8615752
A; Accession: S64709
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C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor
A;Map position: 5q13
A;Introns: 28/1
C;Superfamily: ATP receptor P2u
C;Superfamily: ATP receptor P2u
F;1-36/Domain: activation peptide #status predicted <APT>
F;1-25/Domain: signal sequence #status predicted <SIG>
F;37-397/Product: proteinase-activated receptor 2 #status
                                                                                                                                                A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 29-397 <KAH> A;Cross-references: EMBL:U36753; NC;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DHYVHFSSAVM----GLLFGVPCLVTLVCYGLMARRLYQPLPGSAQSSSRLRS-LRTIAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FHLALSDTLYVLSLPTLIYYYAAHNHWPFGTEICKFVRFLFYWNLYCSVLFLTCISVHRY
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RESULT 7

845680

G protein-coupled peptide receptor EBI 2 - human
C;Species: Homo sapiens (man)
C;Accession: 845680
C;Accession: 845680
R;Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, J. Virol. 67, 2209-2220, 1993
A;Title: Epstein-Barr virus-induced genes: first lymphocyte-specific A;Reference number: A45680; MUID:93188173; pMID:8383238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: B45680
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-361 - GBIR
A;Cross-references: GB:L08177; NID:g292056; PIDN:AAA35924.1;
A;Experimental source: B-lymphocytes
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Best Local Similarity
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Local Similarity 26.9%;
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                                                                                                         L--FVAVLVILIGCYIAISRYIHKSSRQ--FISQSSRKRKHNQSIRVVVAVFFTCFLPYH
                     LCRIPFTFSHLDRLLD-----ESAQKILYYCKEITLFLSAC----NVCLDPIIYFFMCRS
                                                                                                                                                                                                                                                          FRIVHDAGFGPWYFKFILCRYTSVLFYANMYTSIVFLGLISIDRYLKVVKPFGDSRMYSI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RKRAIKLIVTVLAMYLICFTPSNLLLVVHYF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLPEQLLVG-----DMFNYFLSLAIGVFLFPAFLTASAYVLMIRMLRSSAMDENSEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSKLKSPLGVKWHTAVTYVNSCLFVAVLVILIGCYIAISRYI--HKSSRQFISQSSRKRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVQRYWVIVNPMGHSRK-KANIAIGISLAIWLLILLVTIPLYVVKQTIFIPALNITTCHD
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                                                                                                                                                EHAKGVCIFVWILVFAQTLPLLINPMSKQEAERITCMEYPNFEETKSLPW----ILLGAC
                                                                                                                                                                                                                     TRIAYYAMGFDWRIGDALCRITALVFYINTYAGVNFMTCLSIDRFIAVVHPLRYNKIKRI
                                                                                                                                                                                                                                                                                              HHSTARIVMPLHYSLVFIIGLVGNLLALVVIVQNRKKINSTTLYSTNLVISDILFTTALP
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-QHMIKKLRFSNFLECSQR---
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25.9%; Pred. No. 2.6e-22;
tive 70; Mismatches 145
                                                                                                                                                                                                                                                                                                                                                                    74;
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                                                                                                                                                                                                                                                                                                                                                                    Score 345; DB 2; I
Pred. No. 2.9e-22;
74; Mismatches 132;
-HSFQISLHFTVCLMNFNCCMDPFIYFFACKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                first lymphocyte-specific G protein-coupled PMID:8383238
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 361;
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A;Map position: 1p35-1p34.3
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
F;IT-38/Domain: transmembrane #status predicted <TRI>F;54-75/Domain: transmembrane #status predicted <TII>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: the authors translated the codon AAT for residue 316 R;Seyfried, C.E.; Schweickart, V.L.; Godiska, R.; Gray, P.W. Genomics 13, 832-834, 1992
A;Title: The human platelet-activating factor receptor gene (A;Reference number: A42831; MUID:92347886; PMID:1322356
A;Accession: A42831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M80436; NID:g189537; PIDN:AAA60001.1; PID:g189538
A;Experimental source: granulocyte, cell line HL-60 all
R;Nakamura, M.; Honda, Z.; Izumi, T.; Sakanaka, C.; Mutoh, H.; Minami, M.;
J. Biol. Chem. 266, 20400-20405, 1991
A;Title: Molecular cloning and expression of platelet-activating factor rec A;Reference number: A41079; MUID:92041873; PMID:1657923
A;Accession: A41079
                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-226, 'TG', 229-342 <SEY>
A;Residues: 1-226, 'TG', 229-342 <NID:g190697, PIDN:AAA60214.1; PID:g190698
A;Cross-references: GB:M88177; NID:g190697, PIDN:AAA60214.1; PID:g190698
A;Note: sequence extracted from NCBI backbone (NCBIN:109813, NCBIP:109814)
R;Chase, P.B.; Halonen, M.; Regan, J. W.
Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993
A;Title: Cloning of a human platelet-activating factor receptor gene: evidence
A;Reference number: 151923; MUID:93192035; PMID:8383507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:D10202; GB:D90433; NID:g219975; PIDN:BAA01050.1; PID:g219976 R;Sugimoto, T.; Tsuchimochi, H.; McGregor, C.G.A.; Mutoh, H.; Shimizu, T.; Kurachi, Y. Biochem. Biophys. Res. Commun. 189, 617-624, 1992 A;Title: Molecular cloning and characterization of the platelet-activating factor recept A;Reference number: JC1359; MUID:93112021; PMID:1281995 A;Accession: JC1359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M76674; NID:g456293; PIDN:AAA60002.1; PID:g456294 R;Ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochrane, C.G. Biochem. Biophys. Res. Commun. 180, 105-111, 1991 A;Title: Characterization of a human cDNA that encodes a functional rece A;Reference number: JH0479; MUID:92028922; PMID:1656963
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                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-342 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-315,'N',317-342 < SUG>
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J. Biol. Chem. 267, 9101-9106, 1992
A;Title: The human leukocyte platelet-activating factor receptor.
A;Reference number: A40191; MUID:92250505; PMID:1374385
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                                                                                                                                 A;Cross-references: GDB:128806;
                                                                                                                                                         A;Gene: GDB:PTAFR
                                                                                                                                                                                                            A; Cross-references:
                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                             A; Accession: I51923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
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                                                                                                                                                                                                            GB:S56396; NID:g298580; PIDN:AAB25755.1; PID:g298581
                                                                                                                                 OMIM:173393
predicted .
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A; Residues: 1-362 <WEB>
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                                VYSMCTTVFMFCIPFIVILGCYGLIVKALIYKD----LDNSPLRRKSIYLVIIVLTVFAV
                                                                           ----C----LFVAVLVILIGCY-IAISRYIHKSSRQFISQSSRKRKHNQSIRVVVAVFFT 263
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F;134-155/Domain:
F;184-205/Domain:
F;233-253/Domain:
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                                                                                                                                        254 IRVVVAVEFTCELEYHLCRIPETESHLDRLLDESAQKILYYCKEITLELSACNVCLDEII 313
                                                                                                                                                                                                                                                                                           123 IKTAQANTRKRGİS----LSLVIWVAIVGAASYFLILDSTNTVPDSAGSGNVTRCFEHYE
                                                YFFMCRSFSRRLFKKSNIRTRSESIRSLQSVRR 346
                                                                                                                                                                                                                                                                                                                                        F----GDSRMYSITFTKVLSVCVWVIMAVLSLPNIIL--TNGQPT---EDNIHDC----S 193
                                                                                                                                                                                                                                        KLKSPLGVKWHTAVTYVNSCLFVAVLVILIGCYIAISRYIHKSSRQFISQSSRKRKHNQS 253
                                                                                                                                                                                                                                                                                                                                                                                         DMLFLITLPLWIVYYQNQGNWILPKFLCNVAGCLFFINTYCSVAFLGVITYNRFQAVTRP
                                                                                                                                                                                                                                                                                                                                                                                                                                    DLIMTLIFPERIVHDAGEGPWYFKFILCRYTSVLFYANMYTSIVFLGLISIDRYLKVVKP 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHDSSHMDSEFRYTLFPIVYSIIFVLGVIANGYVLWVFARLYPCKKFNEIKIFMVNLTMA
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                                                                                        VCTVLAVFIICFVPHHVVQLPWTLAELG-FQDSKFHQAINDAHQVTLCLLSTNCVLDPVI
                                                                                                                                                                                           KGSVPVLI-IHIFIVF----SFFLVFLIILFCNLVIIRTLLMQPVQQQRNAEVKRRALWM 233
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Pred. No. 6.8e-22;
0; Mismatches 139
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316
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A;Cross-references: EMBL:X73268; NID:g395084; PIDN:CAA51716.1; C;Superfamily: ATP receptor P2u C;Keywords: G protein-coupled receptor; transmembrane protein RESULT 9
\$33733

G protein-coupled receptor - chicken
G;Species: Gallus gallus (chicken)
G;Date: 06-Jan-1995 #sequence_revision
C;Accession: S33733
C;Accession: S3373, Krishek, B.J.;
R;Webb, T.E.; Simon, J.; Krishek, B.J.; A;Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor. A;Reference number: S33733; MUID:93285340; PMID:8508924 A;Accession: S33733 T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, tt. 324, 219-225, 1993 Similarity KVLSVCVWVIMAVLSLPNIILINGQPTEDN----IHDCSKLKSPLGVKWHTAVTYVNS--VHDAGEGPWYFKFILCRYTSVLFYANMYTSIVFLGLISIDRYLKVVKPFGDSRMYSITET FYYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRYTGVVHPLKSLGRLKKKNA 157 FQFYYLPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMFNLALADFLYVLTLPALI FDTIVLPVLYLIIFVASILLNGLAVWIF-FHIRNKTSFIFYLKNIVVADLIMTLTFPFRI 98 Conservative 17.5%; 62; Score 328; DB 2; Pred. No. 8.6e-21; Mismatches 130; 06-Jan-1995 #text_change Indels T.G.; King, B.F.; Burnstoc PID:g395085 50; 24-Sep-1999 Gaps 158 97

TADEYLRSYF

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A; Molecule type: mRNA
A; Residues: 341-363 < CCA2>
A; Gross-references: GB:S67370; NID:g455947; PIDN:AAB29371.1; PID:g455948
A; Experimental source: pituitary
R; Penetta, R; Greenwood, M; Patel, Y.C.
submitted to the EMBL Data Library, August 1993
A; Description: Correction of the nucleotide and amino acid sequence of the A; Reference number: 839244
A; Accession: 839244
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C;Superfamily: vertebrate rhodopsin
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A;Title: Molecular cloning and expression of a pituitary A;Reference number: 157940; MUID:93125499; PMID:1362243
A;Accession: 157940
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A;Residues: 309-363 <PEN>
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A;Residues: 1-363 <OCA1>
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                                                                                                                                                                                                                                                                                                                                                                                          119 VLFYANMYTSIVFLGLISIDRYLKVVKPFGDSRMYSITFTKVLSVCVWVIMAVLSLPNII 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264
                                                                                                                                                                                                                                                                                          179 LTNGQPTEDNIHDCS-KLKSPLGVKWHTA-VTYVNSCLFVAVLVILIGCYIAISRYIHKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
   | ILYYCKEITLFLSACNVCLDFIIYFFMCRSFSRRLFKK
                                                                                                                                                                                                                                                                                                                                                            TLDGINQFTSIFCLMVMSVDRYLAVVHPLRSARWRRPRVAKMASAAVWVFSLLMSLPLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGDTFRRRLSR----ATRKSSRRSEPNVQSKSE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CFLPYHL-----CRIPFTFSHLDRLLDESAQKILYYCKEITLFLSACNVCLDPIIYFF
                                                                                                      AGMRVGSSRRRRSEPKVTRMVVVVVLVFVGCWLPFFIVNIVNLAFT
                                                                                                                                                           SRQFISQSSRKR----KHNQSIRVVVAVFFTCFLPY---HLCRIPFTFSHLDRLLDESAQK
                                                                                                                                                                                                                              FAD---VQEGMGTCNLSWPEPVGL-MGAAFITYTSVLGFFGPLLVICLCYLLIVVKV-KA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTLVI YVVLRHAKMKTVTNVY I LNLAVADVLFMLGLPFLATQNAVVSYWPFGSFLCRLVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGLAVWIFF-HIRNKTSFIFYLKNIVVADLIMTLTFPFRIVHDAGFGPWYFKFILCRYTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSLASTP-----SWNASAASSG-NHNWSLVGSASPMGARAVLVPVLYLLVCTVGLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTLAKLPNNELHGQESHNSGNRSDGPGKNTTLHNEFD----TIVLPVLYLIIFVASILL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62; Mismatches 139;
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Pred. No. 1.1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348
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                                                                                                      -LPEEPTSA
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                                                                            RESULT 12
JC4737
G protein-coupled receptor P2Y1 - human
N;Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor
C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence revision 16-Aug-1996 #text_change 17-Nov-2000
C;Date: 10-May-1996 #sequence revision 554253
C;Date: 10-May-1996 #sequence revision 554253
R;Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.; Boeyn
R;Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.; Boeyn
Biochem Biophys. Res. Commun. 221, 588-593, 1996
A;Title: Cloning and tissue distribution of the human P2Y1 receptor. A;Reference number: JC4737; MUID:96205320; PMID:8630005
A;Accession: JC4737
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A; Residues: 1-373 <HEN>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bovine
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A;Gene: bovp2y

C;Superfamily: ATP receptor P2u

C;Superfamily: ATP receptor P2u

C;Keywords: glycoprotein; phosphoprotein; receptor; transme F;52-77/Domain: transmembrane #status predicted <TM1>
F;88-111/Domain: transmembrane #status predicted <TM2>
F;184-150/Domain: transmembrane #status predicted <TM3>
F;171-191/Domain: transmembrane #status predicted <TM4>
F;171-191/Domain: transmembrane #status predicted <TM4>
F;214-237/Domain: transmembrane #status predicted <TM5>
F;214-237/Domain: transmembrane #status predicted <TM5>
F;305-328/Domain: transmembrane #status predicted <TM5>
F;311,27,113,197/Binding site: carbohydrate (Asn) (covalent)
F;258/Binding site: phosphate (Ser) (covalent) (by protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X87628; NID:g1032484; A;Experimental source: aortic endothelial cell C;Genetics:
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C;Date: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 24-Sep-1999
C;Accession: JC4162
R;Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.
Biochem. Biophys. Res. Commun. 212, 648-656, 1995
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A;Title: Cloning and characterisation of a bovine P2Y receptor
A;Reference number: JC4162; MUID:95352058; PMID:7626079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSRMYSITFTKVLSVCVWVIMAVLSLPNIILTNGQPTEDNIHDCSKLKSPLGVKWHTAVT 208
                                                                                                                                              SIYLVIIVLTVFAVSYIPFHVMKTMNLRARLDFQTPEMCAFNDRVYATYQVTRGLASLNS
                                                                                                                                                                                                             HNQSIRVVVAVFFTCFLPYHLCRIPFTFSHLDRLLDB--SAQKILYYCKEITLFLSACNV 307
                                                                                                                                                                                                                                                                                    CYDTTSDEYLRSYFIYSMCTTVAMFCVPLVLILGCYGLIVRALIYKD----LDNSPLRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYVLTLPALIFYYFNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLK 158
                                                                   CLDPIIYFFMCRSFSRRLFK-----KSNIRTRSESI 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMTLTFPFRIVHDAGFGPWYFKFILCRYTSVLFYANMYTSIVFLGLISIDRYLKVVKPFG 148
CVDPILYFLAGDTFRRRLSRATRKASRRSEANLQSKSEDM
                                                                                                                                                                                                                                                                                                                                                        -----YVNS------CLFVAVLVILIGCY-IAISRYIHKSSRQFISQSSRKRK 249
                                                                                                                                                                                                                                                                                                                                                                                                                                  SLGRLKKKNAVYISVLVWLIV-VVGISPILFYSG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGKNTTLHNEFDTIVLPVLYLIIFVASILLNGLAVWIF-FHIRNKTSFIFYLKNIVVADL
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25.6%;
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Pred. No. 1.3e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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A; Molecule type: DNA
A; Residues: 1-373 < JAN>
A; Cross-references: GB:S81950; NID:g1839438; PIDN:AAB47091.1; PID:g1839439
A; Cross-references: GB:S81950; NID:g1839438; PIDN:AAB47091.1; PID:g1839439
A; Cross-references: GB:S81950; NID:g1839438; PIDN:AAB47091.1; Barnard, E.A.; Kunapuli, R.S.; Barnard, E.A.; K
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A; Molecule: type: mRNA
A; Residues: 1-373 < AYY>
A; Cross-references: GB:U42029; NID:gl147730; PIDN:AAA97872.1; PID:gl147731
A; Cross-references: GB:U42029; NID:gl147730; PIDN:AAA97872.1; PID:gl147731
A; Experimental source: erythro leukemia cells
A; Experimental source: erythro leukemia cells
A; Eachet, C.
R; Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.
R; Leon, C.; Vial, C.; Cazenave, May 1995
submitted to the EMBL Data Library, May 1995
submitted to the EMBL Data Library, May 1995
submitted to the EMBL Data Library, May 1995
A; Reference number: S54253
A; Reference number: S54253
A; Reference number: S54253
A; Recession: S54253
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A;Map position: 3pter-3qter

C;Superfamily: ATP receptor P2u

F;88-11/Domain: transmembrane #status predicted <TM3>

F;174-152/Domain: transmembrane #status predicted <TM6>

F;171-191/Domain: transmembrane #status predicted <TM6>

F;261-282/Domain: transmembrane #status predicted <TM6>

F;261-282/Domain: transmembrane #status predicted <TM7-

C;305-328/Domain: transmembrane #status predicted <TM7-

Covalent) (by protein kinase C) #status predicted predicted predicted phosphate (Ser) (covalent) (by protein kinase C and calmodulin-dependent)

F;330,339/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-dependent)

F;343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-dependent)
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A;Residues: 1-137,139-373 <LEO>
A;Residues: 1-137,139-373 <LEO>
A;Cross-references: EMBL:249205; NID:9798835; PIDN:CAA89066.1; PID:9798836
A;Cromment: This receptor belongs to a family of G protein-coupled receptors. It
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A;Cross-references: GDB:677125;
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Best Local S:
Matches 92
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        354
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h
Similarity 25.3%; Score 325; DB 2; Length 373;
Similarity 25.3%; Pred. No. 1.6e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPGK---NTTLHNE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPLTCISAHRYSGVVYPLKSLGRLKKKNAICISVLVWLIVVVAISP-ILFYSG------ 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HDCSKLKSPLGVKWHTAVT-----YVNS------CLFVAVLVILIGCY-IAIS
                                                                                                                                                                                                                                                                                                                                                                                                RYIHKSSRQFISQSSRKKKHNQSIRVVVAVFFTCFLPYHL-----CRIPFTFSHLDRL 283
        SEDM 357
                                                                                                                                                            LDESAQKILYYCKEITLFLSACNVCLDPIIYFFMCRSFSRRLFK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TĠVRKNKTIŤCYDTTSDEÝLRŚYFIYSMCTTVAMĖCVFĹVLILĠĆÝGLIVR
                                                                                    SESI 338
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                                                                                                                                                                                                                                                                                                                            -LDNSPLRRKSIYLVIIVLTVFAVSYIÞFHVMKTMNLRARLDFQTPAMCAF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OMIM:601167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -FDTIVLPVLYLIIFVASILLNGLAVWIF-FH
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                                                                                                                                                                                                                                                                                          --KSNIRTR 334
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C;Date: 13-Jan-1995 #sequence_revision 10.
C;Accession: A47556
R;Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
R;Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
A;Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.
A;Reference number: A47556; MUID:93281707; PMID:7685114
A;Accession: A47556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:L14751; NID:g309457; PIDN:AAA39871.1; C;Superfamily: ATP receptor P2u C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-373 <LUS>
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                                                                                                                                                                                                                                                                                                                                                        thrombin receptor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I51667
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I51667
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A;Title: Thrombin receptor's specificity for agonist peptide is A;Reference number: 151667; MUID:94195429; PMID:8145852
                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-420 <GER>
                                                                                                                                                                                                                                                                                  A; Reference number:
A; Accession: I51667
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                155
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                                                                                                                                                                   90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAVTYVN----SCLFVAVLVILIGCYIAISRYIHKSSRQFISQSSR-KRKHNQSIRVVVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LHSLRWGRARYARRVAAVVWVLVLACQAPVLYFVTTSVRGTRITCHDTSARE-----LFS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGDSRMYSITFTKVLSVCVMVIMAVLSLPNI--ILTNGQPTEDNIHDCSKLKSPLGVKWH 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HFVAYSSVMLGLLFAVPFSVILVCYVLMARRLLKPAYGTTGGLPRAKRKSVRTIALVLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FALCFLPFHVTR---TLYYSFRSLDLSCHTLNAINMAYKITRFLASANSCLDFVLYF 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FETCETEATHLCKIDETESHLDKLLDESAOKI--LYYCKETTLELSACNYCLDFIIYF 315
                                                                                                                                                                                Similarity
                                                                                                       PERIVHDAGEGEMYEKEILCRYTSVLEYANMYTSIVELGLISIDRYLKVVKPFGDSRMYS
                                                                                                                                   I---TETKVLSVC--VWVIMAVLSLPNIILTNGQ--PTED--NIHDCSKLKSPLGVKWHT 205
                                               Conservative
                                                                                                                                                                     Conservative
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pred. No. 1.8e-20;
pred. No. 1.3e-20;
3; Mismatches 132;
                                                                                                                                                                          59;
                                                                                                                                                                       Score 324.5; DB 2;
Pred. No. 2e-20;
9; Mismatches 133;
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A;Gene: p2Y5

C;Superfamily: ATP receptor P2u

C;Superfamily: ATP receptor P2u

C;Keywords: G protein-coupled receptor; transmembrane protein

F;15-40/Domain: transmembrane #status predicted <TM1>
F;151-74/Domain: transmembrane #status predicted <TM2>
F;89-109/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384
A;Experimental source: T-cells
C;Comment: This receptor plays a role in T-cell activation.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Blochem. Blophys. Res. Commun. 219, 105-110, 1996
A;Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A;Reference number: JC4618; MUID:96190677; PMID:8619790
A;Accession: JC4618
A;Molecule type: mRNA
A;Residues: 1-308 <WEBb
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A;Title: Identification of a G protein coupled receptor induced in activated T cells.
A;Reference number: ISO241; MUID:93329058; PMID:8393036
A;Accession: ISO241
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A; Residues: 1-308 < KAP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Kaplan, M.H.; Smith, D.I.; Sundick, R.S. J. Immunol. 151, 628-636, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 YLYSLLCCRKVSE 388
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                      206 --AVTYVNSCLFVAVLVILIGCYIAISRYIHKS---SRQFISQSSRKRKHNQSIRVVVAV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 IYYPSSFCLLFFFVPFIITTICYIGIIRSLSSSS---IENSCKKTRALFLAVVVLCVFII 323
179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 LSWRTMSRAYMACSFIWLISIASTIPLLVTEQTQKIPRLDITTCHDVLDLKD----LKDFY
                                                                                                                                                                        63 FVFTLÞFRÍYYFV-VRNWÞFGDVLCKISVTLFYTNMYGSÍLFLTCISVDRFLAIVHÞFRS 121
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                                                                                                                                                                                               MTLTFPFRIVHDAGFGPWYFKFILCRYTSVLFYANMYTSIVFLGLISIDRYLKVVKPFGD
                                                                                                                                                                                                                                                                                 NTTLHNEEDTIVLPVLYLIIFVASILLNGLAVWIF---FHIRNKTSFIFYLKNIVVADLI
SRIVIFIEIVGFFIPLILNVTCSTMVLRTLNKPLTLSRNKLS----KKKVLKMIFVHLVI
                                                                                 KTLRTKRNARIVCVAVWITVLAGSTPASFFQSTNRQ---NNTEQRTCFENFPESTWKTYL
                                                                                                                        SRMYSITFTKVLSVCVWVIMAVLSLPNIIL--TNGQPTEDNIHDCSKLKSPLGVKWHT--
                                                                                                                                                                                                                                                   NCSTEDSFKYTLYGCVFSMVFVLGLIANCVAIYIFTFTLKVRNETT--TYMLNLAISDLL
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                   17.2%; Score 321.5; DB 2; Length 308; 27.7%; Pred. No. 2.7e-20;
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#status predicted <TM5>
#status predicted <TM6>
#status predicted <TM7>
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Maximum Match 100%
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 683.692
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Match
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1: sp_archea:*

2: sp_bacteria:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                   sp_rodent:*
sp_virus:*
sp_vertebrate:*
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sp_phage:*
                                                                                                                                                                                                                                                                                                                                          sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                   sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                             sp_invertebrate:*
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                                                                                                                                                                                                                                                     sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
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  1 Q8BG55
Q81V06
1 Q8BY06
1 Q8BTN1
1 Q8BTN1
1 Q8R528
3 Q8F71
1 Q8BY1
1 Q7Z3W3
3 Q7ZZW3
3 Q7ZZW3
3 Q7ZZW3
3 Q7ZZW3
                                                                                                              Q8HXH1
Q8HXH1
Q8CIF3
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Q8iyt7 homo sapien
Q8bzv8 mus musculu
Q8bxh1 macaca fasc
Q8cif3 mus musculu
Q8by65 mus musculu
Q8by65 mus musculu
Q8by70 homo sapien
Q8by85 mus musculu
Q8br11 mus musculu
Q8br28 mus musculu
Q8br528 mus musculu
Q7z3w3 homo sapien
Q7zza4 brachydanio
Q8n587 homo sapien
Q7zwq7 xenopus lae
Q7zxj7 xenopus lae
                                                                                                                                                            Description
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45	44	43	42	41	40	39	38	37	36	35	<u>ب</u> 4	3	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
320.5	320.5	320.5	321	322	322.5	322.5	323.5	323.5	323.5	324	324	325.5	326.5	326.5	329.5	330.5	330.5	332	332	334	334.5	339	346	347	347.5	4	350.5	•
17.1	17.1	17.1	17.1	17.2	17.2	17.2	17.3	17.3	17.3	17.3	17.3	17.4	17.4	17.4	17.6	17.6	17.6	17.7	17.7	17.8	17.8	18.1	8	18.5	18.5	θ.		•
347	347	334	296	373	347	334	358	347	342	359	349	352	390	176	361	369	358	353	342	337	354	342	357	353	341	399	358	357
6	σ	σ	σ	11	0	9	13	σ	0	13	11	0	13	4	11	۲	13	13	σ	4	13	თ	13	13	11	11	13	11
Q9MZN5	Q9MZN6	Q9N1P3	Q9TTY6	Q8BMJ5	Q9MZM7	Q9N130	Q9PUA0	Q9MZM9	Q9XSD4	Q9PVY7	Q8VD47	Q7YS92	Q8QGQ4	Q9BY61	Q8VHP3	Q8ВJВ7	Q9DGI1	Q9PTF7	Q9GK76	Q8IV19	Q7ZWY0	Q9TTY5	Q9DE05	093247	Q8C017	Q8R3I1	Q9YGC3	Q7TMV7
			Q9tty6 canis famil	u	Q9mzm7 callimico g	Q9n130 saimiri bol	Q9pua0 acipenser r	Q9mzm9 ateles pani	Q9xsd4 sus scrofa	7		Q7ys92 tupaia bela	carase	DMO BE	Q8vhp3 cavia porce	Q8bjb7 mus musculu	Q9dgil gallus gall	Q9ptf7 brachydanio	Q9gk76 capra hircu		Q7zwy0 xenopus lae	Q9tty5 bos taurus	Q9de05 raja erinac			Q8r3il mus musculu	Q9ygc3 xenopus lae	Q7tmv7 mus musculu

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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

REMBL; BC034989; AAH34989.1; -.

RG0; GO:0016021; C:integral to membrane; IEA.

RG0; GO:0004872; F:receptor activity; IEA.

RG0; GO:0001584; F:rhodopsin-like receptor activity; IEA.

RG0; GO:0001584; F:rhodopsin-like receptor protein signalin. . .;

RG0; GO:0001584; F:rhodopsin-like receptor prot
                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 147
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QBIYT7;
01-MAR-2003 (TEMBLrel. 23, Created)
01-MAR-2003 (TEMBLrel. 23, Last sequence update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G protein-coupled receptor 105. Homo sapiens (Human).
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                                                                                                                                                                                                                                 Local Sim hes 147;
Similarity
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                       41.0%; Score 768.5; DB 4; Length 47.6%; Pred. No. 1.1e-58; tive 64; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                    338;
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RESULT

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DT O11

O1 O11

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O4 O4 O4

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the RIKEN Genome Exploration Research Group Phase I & II Team;

"Analysis of the mouse transcriptome based on functional annotation o

"To full-length cDNAs.";

"L Nature 420:563-573 (2002).

"R EMBL; AK033448; BAC28294.1; -.

"M MGD; MGI:1918089; P27y12.

"R G0; G0:0001609; F22ry12.

"R G0; G0:0001609; F:adenosine receptor activity, G-protein coupled; IMP.

"G0; G0:0001621; F:platelet ADP receptor activity; IMP.

"G0; G0:0001681; F:platelet ADP receptor activity; IMP.

"G0; G0:0001681; F:platelet ADP receptor activity; IMP.

"G0; G0:0001681; F:platelet ADP receptor.

"G0; G0:0007168; F:platelet activation; IMP.

"G0; G0:0007168; F:platelet activation; IMP.

"G0; G0:00030168; F:platelet activation; IMP.

"G0; G0:000168; F:platelet 
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STRAIN=C57BL/6J; TISSUE=Colon;
MEDLINE=22354683; PubMed=12466851;
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Mammalia; Eutheria;
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01-OCT-2003
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01-MAR-2003
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                                               GLISIDRYLKVVKPFGDSRMYSITFTKVLSVCVWVIMAVLSLPNIILTNGQPTEDNIHDC 192
GLITIDRYLKTTRPEKTSSPSNLLGAKILSVVIWAFMELISLPNMILTNRRPKDKDVTKC
                                                                                                                              KSNFIIFLKNTVISDLLMILTFPFKILSDAKLGAGPLRTLVCQVTSVTFYFTMYISISFL
                                                                                                                                                                                        KTSFIFYLKNIVVADLIMTLTFPFRIVHDAGFGPWYFKFILCRYTSVLFYANMYTSIVFL 132
                                                                                                                                                                                                                                                            DVPGVNTTSANTTFSPGTSTLCVRDYKITQVLFPLLYTVLFPAGLITNSLAMRIFFQIRS
                                                                                                                                                                                                                                                                                                                                DGPGKNTTLHN-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 23, (TrEMBLrel. 23, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                36.9%;
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Last annotation update)
homolog.
                                                                                                                                                                                                                                                                                                                                                                                                 Score 692; DB 11;
Pred. No. 4.9e-52;
0; Mismatches 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 347;
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                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 137; Conserv
                                                                                                                                                                                                                                                      Pfam; PF00001; 7tm_1; 1.
PRINTS; PR01237; GFCRRHODOPSN.
PRINTS; PR01569; PS2Y12PRNCPTR.
PROSITE; PS50262; G PROTEIN_RECEP_F1_2;
Hypothetical protein.
SEQUENCE 342 AA; 39479 MW; 0869FDD01
                                                                                                                                                                                                                                                                                                                                  EMBL; AB097554; BAC41779.1; ...
GC; GO:0016021; C:integral to membrane; IEA.
GC; GO:0045028; F:purinergic nucleotide receptor activity, G-.
GC; GO:001584; F:rhodopsin-like receptor activity; IEA.
GC; GO:0001584; F:rhodopsin-like receptor protein signalin.
InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR005394; P2Y12 purnocptor.
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Q8HXH1;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Medulla oblongata;
MEDLINE=2145851; PubMed=11574149;
Osada N., Hida M., Kusuda J., Tanuma R., Isek
Hirai M., Terao K., Suzuki Y., Sugano S., Has
"Assignment of 118 novel cDNAs of cynomolgus
chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey). Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 275:31-37(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-2002) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Medulla oblongata;
Hashimoto K., Osada N., H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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01-OCT-2003
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KWHTAVTYVNSCLEVAVLVILIGCYIAISRYIHKS--SRQFISQSSRKKKHNQSIRVVVA
                                                            KVVKPFGDSRMYSITFTKVLSVCVWVIMAVLSLPNIILTNGQPTEDNIHDCSKLKSPLGV
                                                                                                                       NIVVADLIMTLTEPERIVHDAGEGPWYFKFILCRYTSVLFYANMYTSIVFLGLISIDRYL 141
                                                                                                                                                                  NRSDGPGKNTTL---HNEFDTIVLPVLYLIIFVASILLNGLAVWIFFHIRNKTSFIFYLK
                                        KTTRPFKTSNPKNLLGTKILSVLIWAFMFLLSLPNMILTNRRPRDKNVKKCSFLKSEFGL
                                                                                            NTVISDLLMILTEPEKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQ
                                                                                                                                                 NLTSAPG-NTSLCTRDYKITQVLFPLLYTVLFFVGLITNSLAMRIFFQIRSKSNFIIFLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 (TrEMBLrel. 23, 0
3 (TrEMBLrel. 23, 1
3 (TrEMBLrel. 25, 1
                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macaca.
                                                                                                                                                                                                                                                         39479 MW; 0869FDD0144A56FC CRC64;
                                                                                                                                                                                                                   36.5%;
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                                                                                                                                                                                                    Score 683.5; DB 6;
Pred. No. 2.6e-51;
9; Mismatches 114;
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EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation updat
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3J databases
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Best Local S
Matches 93
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Q8CIF3;
Q1-MAR-2003
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PRINTS; PR00237; GFCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP_F1_1;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to platelet activating receptor homolog.
F730001G15RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                  Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL, BC024054, AAH24054.1; -. EMBL, BC024054, F730001615Rik.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0001872; F:receptor activity; IEA.

GO; GO:0001874; F:rhddopsin-like receptor activity; IEA.

GO; GO:0001584; F:rhddopsin-like receptor protein sig

GO; GO:0007186; P:G-protein coupled receptor protein sig

InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                 LAIRQLYRNRDNTNYPSVKSAL----LHILLVTASYIICFVPYHAVRIPYTLSQTEVISD
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                                                                                                                                               IMAVLSLPNIILTNGQPTEDNIHDCSKLKSPLGVKWHTAVTYVNSCLFVAV-LVILIGCY
                                                                                                                                                                                YFKFILCRYTSVLFYANMYTSIVFLGLISIDRYLKVVKPFGDSRMYSITFTKVLSVCVWV
                                                                                                                                                                                                               FYLVFLIGIIGSCFATWAFIQKTTNHRCVSIYLINLLTADFLLTLALPVKIVVDLGVAPW
                                                                                                                                                                                                                                  YLIIFVASILLNGLAVWIFFH-IRNKTSFIFYLKNIVVADLIMTLTFPFRIVHDAGFGPW
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                                                            ESAQKILYYCKEITLFLSACNVCLDPIIYFFMCRSF-----
                                                                                                      IAISR-YIHKSSRQFISQSSRKRKHNQSIRVVVAVFFTCFLPYHLCRIPFTFSHLDRLLD
                                                                                                                          MVLLIMVPNMVIPIKDIKEKSNVGCMEFKKEFGRNWHLLTNFICVAIFLNFSVIILISNF
                                                                                                                                                                     KLRIFHCQVTACLIYINMYLSIIFLAFVSIDRCLQLIHSCKIYRIQEPGFAKMISAVVWL
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                     337
317
                                                                                                                                                                                                                                                                                                  319 AA;
                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                  36705 MW; 11E0D6556B694361 CRC64;
                                                                                                                                                                                                                                                                 22.6%;
                                                                                                                                                                                                                                                         63;
                                                                                                                                                                                                                                                     Score 423; DB 11; Length : Pred. No. 1e-28; Indels 3; Mismatches 129; Indels
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RESULT 6
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Best Local S
Matches 92
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EMBL; AK089287; BAC40829.1; -.
EMBL; AK089287; BAC40829.1; -.
EMGD; MGI:2442043; F730001G15Rik.
GO; GO:0016021; C:integral to membrane; IBA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IBA.
GO; GO:0007186; P:G-protein coupled receptor protein sig
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable G protein-coupled receptor H963 homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8BG55;
                                                                                                     Q8IV06; PRELIMINARY;
Q8IV06;
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00001; 7tm_1; 1.—
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
SEQUENCE 319 AA; 36719 MW; C2EODE58FB694364 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The FANTOM Consortium,
the RIKEN Genome Exploration Research
"Analysis of the mouse transcriptome b
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                 Platelet activating receptor homolog. Homo sapiens (Human).
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
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R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0016021; F:receptor activity; IEA.

R GO; GO:000184; F:receptor activity; IEA.

R GO; GO:0001864; F:receptor activity; IEA.

R GO; GO:0007186; F:G-protein coupled receptor protein s:

R GO; GO:0007186; GP-protein RECEP_F1 1; 1.

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NCBI_TaxID=9606;
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   the RIKEN Genome Exploration Research Group Phase I & II

"Analysis of the mouse transcriptome based on functional

60,770 full-length cDNAs.";

10,770 full-length cDNAs.";

11, Nature 420:563-573 (2002).

12 EMBL; AK041582; BAC30993.1;

13 EMBL; AK041582; BAC30993.1;

14 GO; GO:0016021; C:integral to membrane; IEA.

15 GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

16 GO; GO:0001586; F:G-protein coupled receptor protein sig.

17 GO; GO:0001786; P:G-protein coupled receptor protein sig.

18 GO; GO:0007186; P:G-protein coupled receptor protein sig.

18 GO; GO:0007186; P:G-protein coupled receptor protein sig.

18 GO; GO:0007186; P:G-protein coupled receptor protein sig.
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Q8BY85;
01-MAR-2003
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STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
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Mammalia; Eutheria;
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pred. No. 2.1e
55; Mismatches
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, Last annotation update)
receptor H963 homolog
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Sciurognathi; Muridae; Murinae; Mus.
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PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1 2;

PROSITE; PS50262; G_PROTEIN_RECEP_F1 2;

PROSITE; PS50262; G_PROTEIN_RECEP_F1 2;

PROSITE; PS50262; G_PROTEIN_RECEP_F1 2;
Query Match
Best Local S
Matches 92
                                                                                                      Nature 420:303 BAC40815 1;

EMBL; AK089252; BAC40815 1;

MGD; MGI:2442043; F730001d15Rik.

MGD; MGI:2442043; F730001d15Rik.

GO; GO:0001584; F:rhodopsin-like receptor protein s:

GO; GO:0001584; F:rhodopsin-like receptor protein s:

GO; GO:0001586; P:G-protein coupled receptor protein s:

GO; GO:0007186; P:G-protein coupled receptor protein s:

GO; GO:0007186; P:G-protein RECEPT1 1:

PFAm; PF000017; Tem 1:

PFAm; PF000017; GPCRRHODDSN

PROSITE; PS000237; GPROTEIN RECEPT1 2:

PROSITE; PS000237; GPROTEIN RECEPT1 2:

RECORDINGE 317 AA; 36450 MW; 84D57352291B5A1E CRC64;
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01-MAR-2003
01-MAR-2003
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Mammalia; Eutheria; Rodentia;
NCBI TaxID=10090;
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01-OCT-2003 (TrEMBLrel.
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STRAIN=NOD;
STRAIN=22354683; PubMed=12466851;
MEDLINE=22554683; PubMed=12466851;
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the RIKEN Genome Exploration Research Group
the RIKEN Genome Exploration Research based o
"Analysis of the mouse transcriptome based o
"Analysis of the mouse transcriptome based o
60,770 full-length cDNAs.",
80,700 full-length cDNAs.",
Nature 420:563-573 (2002)
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pred. No. 2.3e-28;
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Sciurognathi; Muridae;
                        Score 417; DB 11;
pred. No. 3.4e-28;
pred. No. 3.4e-129;
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"Mouse CysLT2 Gene.";
submitted (MAR-2001) to the EMBL/GenBank/DDBJ dat
EMBL; AB058930; BAB86881.1; -.
EMGD; MGG1:1917336; CysLte12
EGO; GO:0001631; F:cysLte11y1 leukotriene receptor
InterPro; IPR004071; CysLeuk_receptor.
InterPro; IPR004071; CysLeuk_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PP00001; 7tm 1; 1.
R PRINTS; PR01533; CYSLTRECPTR.
R PRINTS; PR01533; CYSLTRECPTR.
R PRINTS; PS0262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
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SEQUENCE
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Q8R528;
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01-JUN-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cysteinyl leukotriene 2 CYSLTR2.
                                                                                                                                                                                                                                                                                                                                                   102;
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                                                                                                                                                                                                                                                                                                                                                                  Similarity
MAVLSLPNIILTNGQPTEDNIHDCSKLKSPLGVKWHTAVTYVNSCLFVAV-LVILIGCYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YLIIFVASILLNGLAVWIFFHIRNKTSFIFYLKNIVVADLIMTLTFPFRIVHDAGFGPWY
                                                       KFKSLL-IMNHIAV----AVGFLLPFLTLTICYLLIRILLKAE---IPESGPRAAHRKA
                                                                                         KLKSPLGVKWHTAVTYVNSCLFVAVLVILIGCYIAISRYIHKSSRQFISQSSRKRKHNQS
                                                                                                                               ATVHPF--
                                                                                                                                                              KVVKPFGDSRMYSITFTK---VLSVCVMVIMAVLSLPNIILTNGQPTEDNIHDC-----S
                                                                                                                                                                                                  NLATSDFLFISTLPFRADYYFRGSNWIFGDLACRVMSYSLYVNMYTSIYFLTVLSVVRFL
                                                                                                                                                                                                                                                                           TGTPSSYSNRNCTIEN-FKKEFYPIIYLIIFFWGALGNGFSIYVFLQTCKKSTSVNVFML
                                                                                                                                                                                                                                                                                                           SGNRSDGPGKNTTLHNEFDTIVLPVLYLIIFVASILLNGLAVWIFFH-IRNKTSFIFYLK 81
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                                                                                                                                                                                                                                                                                                                                                                                                                          309 AA;
                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                             -RMFHVTSVRSAWILCGIIWVF--IMASSALLLVNGQEEKDNIISCLELSPQ
                                                                                                                                                                                                                                                                                                                                                                                                                          35226 MW;
                                                                                                                                                                                                                                                                                                                                                                  20.4%; Score 381.5; DE 31.5%; Pred. No. 4e-25;
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                                                                                                                                                                                                                                                                                                                                                   56;
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   PRELIMINARY;
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PRINTS; PR00237; GPCKRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98086419; PubMed=9415702;
Boyer J.L., Waldo G.L., Harden T.K.;
"Molecular cloning and expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Pharmacol. 52:928-934(1997).

EMBL, AF031897; AAC60339.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity;

GO; GO:0001584; F:rhodopsin-like receptor proteir

GO; GO:0007186; P:G-protein coupled receptor proteir

InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagri
NCBI_TaxID=9103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00001; 7tm_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 GKNTT-----LHNEFDTIVLPVLYLIIFVASILLNGLAVWIFF-HIRNKTSFIFYLK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                      GVKWHTAVTYVNS---CLFVAVLVILIGCYIAISRYIHKSSRQFISQSSR----KRKHNQ
                                                                                                                                                                                                                                                                                                                                                                                                 NIVVADLIMTLTFFFRIVHDAGFGFWYFKFILCRYTSVLFYANMYTSIVFLGLISIDRYL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGNTTAAAEAKCVFNEEFKFILLPISYGIVFVVGLPLNSWAMWIFVSRMRPWNATTTYMF
                                                                                      MIIIVLTVFAICFVFFHITR---TLYYTSRYFQADCOTLNIINFTYKITRPLASINSCLD
                                                                                                                                SIRVVVAVFFTCFLPYHLCRIPFTFSHLDRLLDESAQ--KILYYCKEITLFLSACNVCLD
                                                                                                                                                                                                                                                                   GICHPIRSLKWVKTKHARLICVGVWLVVTICLIPNLIFVTTSSKDNSTLCHDTTKPE---
                                                                                                                                                                                                                                                                                                             KVVKPFGDSRMYSITFTKVLSVCVWVIMAVLSLPNIIL--TNGQPTEDNIHDCSKLKSPL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFLYYFAGENFKARLRAIFSKVHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIIYFFMCRSFSRRL---FKKSNI
PILYFMAGDKYRGRLRRGAAQRPR
                                          PIIYFFMCRSFSRRLFKKSNIRTR
                                                                                                                                                                            --EFDHYVHYSSSIMALLFGIPFLVIVVCYCLMAKRLCK--RSFPSPSPRVPSYKKRSIK
                                                                                                                                                                                                                                                                                                                                                           NLAISDTLYVFSLPTLVYYYADRNNWPFGKVFCKIVRFLFYANLYSSILFLTCISVHRYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTTIVIAMITELLCFLPYHALRT----LHLVTWDKDSCGDVLHKATVITLTMAAANSCFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42594 MW; 849C465722BDD02B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.0%; Score 374; DB 13; 29.3%; Pred. No. 2.2e-24; tive 67; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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annotation updat
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                                            334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30;
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                                                                                                                                                                               254
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PRT;

375

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STRAIN=C57BL/6J, TISSUE=Spinal cord;

KMEDLINE=22354683; PubMed=12466851;

KMEDLINE=22354683; PubMed=12466851;

KMEDLINE=22354683; PubMed=12466851;

The PARTOM Consortium,

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Best Local Similarity 29.6%;
Matches 102; Conservative 6
RESULT 12
Q7Z3W
ID Q7Z3W
AC 07Z3W
AC 07Z3W
OT 01-0C
DT 01-0C
DT 01-0C
DT Hypot
GN Hypot
GN Homo
OS Homo
OC Mammae
OX NCBI
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
probable G protein-coupled receptor GPR34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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PÉAM; PF00001; 7tm 1; 1.

PRINTS; PR00237; GFCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS00262; G PROTEIN RECEP F1 2; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                           Q7Z3W3
Q7Z3W3;
Q1-OCT-2003
Q1-OCT-2003
Q1-OCT-2003
                   Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; l
                                                                         Hypothetical F
DKFZP686N1782.
 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YTSIVELGLISIDRYLKVVKPFGDSRMYSITETKVLSVC--VWVIMAVLSLPNIILT--- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEHI-RNKTSEIEYLKNIVVADLIMTLTFPERIVHDAGEGDWYFKEILCRYTSVLEYANM 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QFISQSSRKRKHNQSIRVVVAVFFTCFLPYHLCRIPFTFSHLDRLLDESA---QKILYYC 295
                                                                                                                                                                                                                                                                                                                                                                                                                       GGH----NSTMCFHYRDRHNAKGEAIFNFYLVVMFWLIFLLIİLSYİKİGKNLLRIPKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGQPTEDNIHDCSKLKSPLGVKWHTAVTYVNSCLFVAVLVILIGCYIAISRYIHK--SSR
                                                                                                                                                                                                                                                                                                      KEITLELSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTRSESIRS 340
                                                                                                                                                                                                                                                                              375 AA;
                                                                                           (TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation updat
(TrEMBLrel. 25, Greated)
                                                                                                                                                                                         PRELIMINARY;
                             Chordata;
primates;
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Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 369;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                   PRT;
                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                     376
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5.9e-24;
                                                                                                                                                                                                      B
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                                                                                                                               update)
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Query Match
Best Local S
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Q7ZZA4
                                               Matches
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TISSUB-Human retina; D., Mewes H.W., Weil B., I
Wambutt R., Heubner D., Mewes H.W., Weil B., I
Fobo G., Han M., Wiemann S.;
Fobo G., Han M. Other EMBL/GenBank/DDBJ
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical SEQUENCE 37
                                                                        Submitted (represented by State 1 to membrane; IEA.

EMSL; AL590151; CAD580671; -

GO; GO:00016021; C:integral to membrane; IEA.

GO; GO:0001872; F:receptor activity; IEA.

GO; GO:0001864; F:receptor activity: IEA.

GO; GO:0007186; F:receptor in coupled receptor protein sign; GO:0007186; P:G-protein coupled receptor protein sign; InterPro; IPR000276; GPCR_Rhodpsn.

PERMIS; PR000217; GPCREHODOPSN.

PRINTS; PR00237; GPROTEIN_RECEP_F1_1; 1.

R PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

R PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
Query Match
Best Local S
Matches 99
                                                                                                                                                                                                                                                                                                                                    07ZZA4
07ZZA4;
01-JUN-2003
01-JUN-2003
01-OCT-2003
                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertu
Actinopterygii; Neopterygii; Teleostei; Osta:
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                            SI:bZ46J2.9
SI:BZ46J2.9.
                                                                                                                                                                                                 Submitted (FEB-2003) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              NCBI_TaxID=7955;
                                                  Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 KNATMGYLTSSLSTKLIPAIYLLVEVVGVPANAVTLWMLFERTRSICTTVEY-TKLAIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNTT---LHNBEDŢIVLPVLYLIIFVASILLNGLAVŅ-IŖŖHIŖNKTSFIŖYLKŅIVVĀŅ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDSRMYSITETKYLSVCYMVIMAVLSLÞNILLING----QÞ---TEDNIHDCSKLKSÞIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VKWHTAVTYVNSCLEVAVLVILIGCYIAISRYIHKSSRQFISQSSRKRKHNQSIRVVVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYRGLEKHTYALVTCGLVNATVELYMLEFFİLKQBYYLVQEDITTCHDVHNTCESSSEFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYYFISLAFFG---FLIPFVLIIYCYAAIIRTLNAYDHRWL-----WYVKASLLILVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al protein.
376 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.7%;
milarity 28.6%;
Conservative 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EETCETBAHTCE1----BELESHTDETTDESWOKITAACKELTFETSWCWACTDELLAEE 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MCRSFSRRLFKKSNIRTRSESIRSLOSVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTICEAPSNIILIIHHANYYYNNTDG------LYFIYLIALCLGSLNSCLDPFLYFL
    Similarity
99; Conserv
                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
(Novel protein similar to nucleotide re
                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                       347
                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42720 MW;
                                                         39861 MW;
                    19.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -KTRNHSTAYLTIVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 369; DB 4;
Pred. No. 5.9e-24;
5; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7638373C15A695DD
                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
          Score 368.5; DB 13;
pred. No. 6.1e-24;
2; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        369; DB 4;
No. 5.9e-24;
                                                          3D3C01F83CC283E2
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Ostariophysi; Cypriniformes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                    protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                          receptors)
                                                                  CRC64;
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                    Indels
                                           Length
                                                                                                                                                                      IEA.
                                                                                                                                                       signalin.
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                        31;
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147
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                                                                                                                                                               IEA.
                            11;
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Conservative

62;

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QBN5S7
ID QBN5S
AC QBN5S
AC QBN5S
AC QBN5S
AC QBN5S
AC QBN5S
AC QBN5S
AC QBN5S
AC QBN5S
AC QBN5S
AC QBN6D
AC OC BUAB
AC AC BUAB
AC AC BCAB
AC AC BCAB
AC AC BCAB
AC AC BCAB
AC AC BCAB
AC AC BCAB
AC AC BCAB
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Best Local S
Matches 95
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Q8N5S7;
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor.
SEQUENCE
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PRINTS; PR00237; GFCRRHODDPSN.

PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
G protein-coupled receptor 17.
Homo sapiens (Human)
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
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TISSUE-Brain, and Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
L; BC031653; AAH31653.1; -.
GO:0016021; C:integral to membrane; IEA.
GO:0004872; F:receptor activity; IEA.
GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO:0007186; P:G-protein coupled receptor protein sig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243
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                                                                                                                                                                                                                  MTLTEPERIVHDAGEGPWYEKFILCRYTSVLFYANMYTSIVFLGLISIDRYLKVVKPFGD
                                                                                                                                                                                                                                                                                      GQETPLEN----MLFASFYLLDFILALVGNTLALWFFIRDHKSGTPANVFLMHLAVADLS
                                                                                                                                                                                                                                                                                                              GKNTTLHNEFDTIVLFVLYLIIFVASILLNGLAVWIFFH-IRNKTSFIFYLKNIVVADLI 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AICFVPPHITR---TLYYAYRIFDADCKTLNIVNFSYKITRPLASVNSCLDPILYFLAGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FPFRIVHDAGFGPWYFKFILCRYTSVLFYANMYTSIVFLGLISIDRYLKVVKPFGDSRMY 153
                                                     LKLRRPLYAHLACAFLWVVVAVAMAP--LLVSPQTVQTN------HTVV--
                                                                                                                                                                     CVLVLPTRLVYHPSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIVHPVKS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYRSKLLRVLTRQTPNTRS 318
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                                                                                                          SRMYSITFTKVLSVCVWVIMAVLSLPNIILTNGQPTEDNIHDCSKLKSPLGVKWHTAVTY 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -CRSFSRRLFKKSNIRTRS 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFDEEFKYILLPVSYSLVCFFGLILNSVALWMFITKMRPWKPSTVYMFHLALSDTLYVLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 AA;
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Pred. No. 8.8e-23;
--- FVAVLVILIGCYIAISRYIHKSSRQFISQSSR-KRKH
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC046837; AAH46837.1; -.

R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:001584; F:rhodopsin-like receptor activity; IEA.

R GO; GO:0007186; P:G-protein coupled receptor protein signalin. ..

R GO; GO:0007186; P:G-protein coupled receptor protein signalin. ..

R GO; GO:0007186; P:G-protein coupled receptor protein signalin. ..

R GO; GO:0007186; P:G-protein coupled receptor protein signalin. ..

R GO; GO:0007186; P:G-protein coupled receptor protein signalin. ..

R PARINTS; PR00237; G-PROTEIN RECEP F1 1; 1.

R PROSITE; PS00237; G-PROTEIN RECEP F1 2; 1.

W Hypothetical protein.

Q SEQUENCE 537 AA; 61981 MW; B030F67D76CB9622 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7ZWQ7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
 331
                                                                    276
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                                                                                                                                                                                                                                                                       101 YYYADKNNWPFGEVLCKLVRFLFYANLYSSILFLTCISVHRYRGVCHPITSLRRMNAKHA 160
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                                 NIRTRS 335
                                                                                                                                                                                                                                      KVLSVCVWVIMAVLSLPNIILINGQPTEDN--IHDCSKLKS-PLGVKWHTAVTYVNSCLF
TVRRRS
                                                                                                  RIPFTFSHLDRLLDES--AQKILYYCKEITLFLSACNVCLDPIIYFFMCRSFSRRLFKKS
                                                                                                                                                                   VAV-LVILIGCYIAISRYIHK---SSROFISQSSRKRKHNOSIRVVVAVFFTCFLPYHLC 271
                                                                                                                                                                                                      YVICALVWLSVTLCLVPNLIFVTVSPKVKNTICHDTTRPEDFARYVEYSTAI----MCLL
                                                                                                                                                                                                                                                                                         VHDAGFGPWYFKFILCRYTSVLFYANWYTSIVFLGLISIDRYLKVVKPFGDSRWYSITFT 158
                                                                                                                                                                                                                                                                                                                                         PKFLLLPVSYSAVFMVGLPLNIAAMWIFIAKMRPWNPTTVYMFNLALSDTLYVLSLPTLV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOSIRVVVAVFFTCFLPYHLCRIPFTFSHLDRLLDESAQKILYYCKEITLFLSACNVCLD
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                                                                                                                                                                                                                                                                                                                                                                        PDTIVLPVLYLIIFVASILLNGLAVWIFF-HIRNKTSFIFYLKNIVVADLIMTLTFPFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIIYFFMCRSFSRRL 325
                                                                  R---TLYYYARLLGIKCYALNVINVTYKVTRPLASANSCIDPILYPLANDRYRRRLIR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIMYFFVAEKFRHAL 308
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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336
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                                                                                                                                                                                                                                                                                                                                                                                                           58;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 352; DB 13;
Pred. No. 2.5e-22;
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodengran B.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Willialon D.K., Muzny D.M., Sodengran B.J., Lu X., Gibbs R.A.,
RA Willialon D.K., William J.W., Green E.J., Dickson M.C.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
Proc. Natl. Rod. Sci. U.S. A. 99:16899-16903 (2002).
 Matches 358;
                            Query Match
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CONFLICT
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                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                        Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GFCRHODOPSN.
PRINTS; PR01735; P2Y13PRNCPTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 6063/9; -.

GO; GO:0016021; C:integral to membrane; NAS.

GO; GO:0016526; F:G-protein coupled receptor activity, unknow.

InterPro; IPR000276; GPCR_Rhodpsn.

InterPro; IPR008109; P2Y13_purnocptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF411114; AAL26485.1; -
EMBL; AK027784; BAB55366.1; -
EMBL; AF945566; AAK29069.1; ALT_INIT.
EMBL; BC009540; AAH09540.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF237763; AAK01858.1; -. EMBL; AF411114; AAL26485.1; -. EMBL; AK027784; BAB55366.1; -.
                                                                                                                                                           TRANSMEM
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                                                                                                                                                                                                                                                                         FRANSMEM
                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Expressed in placenta and prostate
expression in thymus. Not expressed in thalamus, hippoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or cerebellum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Orphan receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       606379;
                 Similarity
                                                        4
25
33
154
358 AA;
  Conservative
                                                                                                                                                                                                                              148
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N-LINKED (GLCNAC. ..) (POTENTIAL)
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Score 1874;
Pred. No. 7.9
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CYTOPLASMIC (
                                                                                                                              BY SIMILARITY.
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             DB 1;
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RESULT 2
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ID GP87_MOUSE
             RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Satto R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Satto R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
Ra Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
Ra Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
Ra Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Gasterland T., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanai A., Kwayii H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Nagashima T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald K.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Hayateu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
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10-OCT-2003 (Rel. 4
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MEDLINE=22354683;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MGD; MGI:193413; Gpr87.

InterPro; IPR000276; GPCR_Rhodpsn.

InterPro; IPR008109; P2Y13_purnocptc

Pfam; PF00001; 7tm 1; 1.

PFRNTS; PR00237; GPCRHODDSN.

R PRINTS; PR01735; P2Y13PRNCPTR.

R PROSITE; P800237; G_PROTEIN_RECEP;

PROSITE; PS0262; G_PROTEIN_RECEP;

TAGGET PS50262; G_PROTEIN_RECEP;
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Best Local
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"Analysis of the mouse transcriptome 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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PROTEIN_RECEP_F1_2; 1.
ecceptor; Transmembrane; Glycoprotein.
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EXTRACELLULAR (POTENTIAL).
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RESULT 3
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15-UUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
UDP-glucose receptor (G protein-coupled recep
GPR105 OR KIAA0001.
Homo sapiana ''
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20219108; PubMed=10753868;
Chambers J.K., Macdonald L.E., Sarau H.M., Ames R.S., Freeman Poley J.J., Zhu Y., McLaughlin M.M., Murdock P., McMillan L., Trill J., Swift A., Aiyar N., Taylor P., Vawter L., Naheed S., Szekerse P., Hervieu G., Scott C., Watson J.M., Murphy A.J., D. Klein C., Bergsma D.J., Wilson S., Livi G.P.;
NA G protein-coupled receptor for UDP-glucose.";
J. Biol. Chem. 275:10767-10771 (2000).
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Q15391;
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         GO; GO:0016021; C:integral to membrane; NAS. GO; GO:0045029; F:UDP-activated nucleotide re GO; GO:0007186; P:G-protein coupled receptor InterPro; IPR000276; GPCR Rhodpen. InterPro; IPR002466; UDPG_receptor.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                           EMBL; D13626; BAA02791.1; -.
EMBL; AF456925; AAL47764.1; -.
Genew; HGNC:16442; GPR105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mutations in a novel gene with transmembrane domains underlie Usher syndrome type 3."; Am. J. Hum. Genet. 69:673-684(2001).
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                                                                                                                                                                                          or send an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96051387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 275:10767-10771(2000).

FUNCTION: Receptor for UDP-glucose and other UDP-sugar coupled G-proteins. Not activated by ATP, ADP, UTP or ATP.

SUBCELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: Highest expression in the placenta, adipose tissue, stomach and intestine, intermediate levels in the brain spleen, lung and heart, lowest levels in the kidney.

SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                                                     receptor activity; NAS. or protein signalin. . .
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Best Local S
Matches 147
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CARBOHYD
CARBOHYD
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PROSITE; PS00237; G PROTEIN RECEP F1 1; FALSE NEGROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 1; FALSE NEGROSITE PROTEIN RECEP F1 1; FALSE NEGROSITE PROTEIN RECEP F1 1; FALSE NEGROSITE PROTEIN RECEP F1 1; FALSE NEGROSITE PROTEIN RECEP F1 1; FALSE NEGROSITE PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN P
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                                                  SEQUENCE FROM N.A.
Lee B.C., Scadden
                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                 Q9ESG6;
28-FEB-2003
                                                                                                                                                                                                                                                                                       P2YX
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TRANSMEM
                                 "7 transmembrane G protein coupled receptor from hematopoietic
                                                                                                                                                                                          UDP-glucose
                                                                                                                                                                                                                15-MAR-2004
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(Rel. 41, Last sequence update)
(Rel. 43, Last annotation updat
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47.6%;
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protein-coupled receptor GPR105).
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EMBL/GenBank/DDBJ databases
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Pred. No. 1.
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N-LINKED (GLCNAC. ..) (POTENTIAL)
, BDBE7C782CB4753D CRC64;
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EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
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7 (POTENTIAL).
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6 (POTENTIA)
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                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                   PRT;
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RN [2]

RN SEQUENCE FROM N.A.

PROBLINE=22388257; PubMed=12477932;

RC TISSUE=01factory epithelium;

RC TISSUE=2388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L.S. Shenmen C.M., Schuler G.D.,

RA Altechal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan R.D., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Willalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Parishman T.W. Green R.D. Dickson M.C.,
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whiting M., Madan A., 10419 A.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-leng
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                     DOMAIN
DISULFID
                                                                                                                                     TRANSMEM DOMAIN TRANSMEM
                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01655; UDPGLUCOSER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:2155705; Gpr105.
GO; GO:0016021; C:integral to membrane; ISS.
GO; GO:0045029; P:UDP-activated nucleotide receptor activity; I
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR005466; UDPG_receptor.
                                                   SEQUENCE
                                                                     CARBOHYD
                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF177211, AAG09275.1; -. EMBL; BC058558; AAH58558.1; -.
                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                     338
                                                                                                     38861
 39.6%;
44.0%;
                                                     WW;
                                                 CYTOPLASMIC (POTENTI
BY SIMILARITY.
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
W; 4376B50622A6BA4E C
                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Glycoprotein.
EXTRACELLULAR (POTENTIAL).
 Score 742.5;
Pred. No. 6e-
                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                     5 (POTENTIAL)
CYTOPLASMIC (
                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
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2 (POTENTIA)
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                                                                   (GLCNAC. . .)
                                                                                                                       (POTENTIAL)
                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
DB
-42;
                                                       CRC64;
                 Length 338;
                                                                                       (POTENTIAL)
                                                                     (POTENTIAL).
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RESULT 5
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Q9EPX4;
    EMBL; AF313450; AAG48945.1; -.
InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR005394; P2Y12 purnocptor.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01569; P2Y12PRNCPTR.
PROSITE; P$00237; GPROTEIN RECEP_F1 1; FALSE_NEG_PROSITE; P$00237; GPROTEIN RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycopi
                                                                                                                                                                                                                                                                                                                           STRAIN-Sprague-Dawley;
MEDLINE-21037966; PubMed=11196645;
Hollopeter G., Jantzen H.-M., Vincent D.
Ramakrishnan V., Yang R.-B., Nurden P.,
                                                                                                                                                                                                                                                                                                                                                                                                              P2RY12.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Eukaryota; Eutheria; Rodentia;
                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation update)
P2Y purinoceptor 12 (P2Y12) (P2Y12 platelet A
                                                                                                                                                                                                                                                                                antithrombotic drugs.";
Nature 409:202-207(2001).
                                                                                                                                                                                                                                                                                                                    Conley P.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                        "Identification of the
                                                                                                                                                                                                                     SUBCELLULÂR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                         FUNCTION: Receptor for ADP inhibit the adenylyl cyclas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KWHTAVTYVNSCLFVAVLVILIGCYIAISRYIHKS---SRQFISQSSRKRKHNQSIRVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVVKPFGDSRMYSITFTKVLSVCVWVIMAVLSLPNIILTNGQPTEDNIHDCSKLKSPLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSGNRSDGPGKNTTLHNEFDTIVLPVLYLIIFVASILLNGLAVWIFFHIRNKTSFIFYLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QPFREVLNKKLHMSLKVQNDLEVSKTKRENA - - IHESTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSFSRRLFKKSNIRTRSESIRSLQSVRRSEVRIYYDYTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVFVVCFVPYHIARIPYTKSQTEGHYSCRTKETLLYAKEFTLLLSAANVCLDPIIYFFLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KWHKASNYIFVSIFWVVFLLLIVFYTAITRKIFKSHLKSRK--NSTSVKRKSSRNIFSIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIVVADELMGLTEPEKVLGDSGLGPWQVNVEVCRVSAVIEYVNMYVSIVEFGLISEDRYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNSTTTDPENQPCSWNTLITKQIIPVLYGMVFITGLLLNGISGWIFFYVPSSKSFIIYLK
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Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                        receptor
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       Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor)
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., Julius D.J.,
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c system (By
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Best Local
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Hippocampus, and Testis;

STRAIN=C57BL/6J; TISSUE=Hippocampus, and Testis;

STRAIN=21085660; PubMed=11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Kawai J., Shinagawa A., Shibata K., Yoshino M., Adachi J., Fukuda Arakawa T., Hara A., Pukunishi Y., Komno H., Kondo S., Yamanaka Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Fleischmann W., Gaasterland T., Nikaido I., Pesole G., Quackenbu
                                                                                                                                                                                                            Q9CPV9;
28-FEB-2003
28-FEB-2003
10-OCT-2003
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TRANSMEM
DOMAIN
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P2YC_N
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SEQUENCE
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TRANSMEM
                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                         Mus musculus
                                                                                                                                                                                     P2RY12
                                                                                                                                                                                               P2Y purinoceptor
                                                                                                                                                                                                                                                                                  6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFFTCFLFYHLCRIFFTFSHLDRLLDESAQKILYYCKBITLFLSACNVCLDFIIYFFMCR
                                                                                                                                                                                                                                                                                                                                                                                                                  VKWHTAVTYVNSCLEVAVLVILIGCYIAISRYIHKS-SRQFISQSSRKRKHNQSIRVVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKVVKPFGDSRMYSITFTKVLSVCVWVIMAVLSLPNIILTNGQPTEDNIHDCSKLKSPLG
                                                                                                                                                                                                                                                                                                                    SFRNSL
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                                                                                                                                                                                                                                                                                                                                                                    LKTTRPFKTSSPSNLLGAKILSVAIWAFMFLLSLPNMILTNRRPKDKDITKCSFLKSEFG
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                                                                                                                                                                         (Mouse)
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A
                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                      315
                                                                                                                                                                                                                                                                                                                                            325
                                                                                                                                                                                                           41, Created)
41, Last sequence up
42, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
39047
                                                                                                                                                                                                 (P2Y12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.4%;
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6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

N.LINKED (GLCNAC...) (PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 700.5; DB 1;
Pred. No. 3.4e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
; 7AE0AFCE66674136 CRC64;
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5 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC 4 (POTENTIAL)
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3 (POTENTIAL)
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                                                                                                                                                Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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                                                                                                                                                              Euteleostomi;
                                                                                                                                                 Murinae;
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Gaps

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ak Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Ak Altachul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Ak Altachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Ak Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Ak Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Ak Hopkins R.F., Jordan H., Moore T., Rubin G.M., Hong L.,

Ak Hopkins R.F., Jordan K., Farmer A.A., Rubin G.M., Hong L.,

Ak Hopkins R.F., Jordan R., Farmer A.A., Rubin G.M., Hong L.,

Ak Hopkins R.F., Jordan R., Farmer A.A., Rubin G.M., Hong L.,

Ak Brownstein M.J., Usdin T.B., Toshiyuki S., Carainci P., Prange C.,

Ak Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Ak Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Ak Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Ak Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Ak Allalon D.K., Walan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Ak Allalon D.K., Touchman J.W., Green E.D., Dickson M.C.,

Ak Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Ak Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ak Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ak Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ak Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ak Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ak Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ak Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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Ak Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ak Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ak 
G-protein
DOMAIN
TRANSMEM
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                 PROSITE;
                                                                                                                                                                                           MGD; MGI:1918089; P2ry12.

GO; GO:0005897; C::Integral to plasma membrane; IC.
GO; GO:0001609; F:ademosine receptor activity; G-protein coupled; IMP.
GO; GO:0001621; F:platelet ADP receptor activity; IMP.
GO; GO:0001188; P:G-protein signaling, coupled to cAMP nucleo. ..; IMI
GO; GO:0030168; P:Platelet activation; IMP.
InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR005394; P2Y12 purnocptor.
Pfam; PF00031; GFCRHODOPSN.
PRINTS; PR00337; GFCRHODOPSN.
PRINTS; PR00337; GFCRHODOPSN.
PRINTS; PR00337; GFCRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AK013804; BAB29000 1; -.
EMBL; AK014807; BAB59561.1; -.
EMBL; BC025428; AAH25428.1; -.
EMBL; BC027381; AAH27381.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibit the adenylyl cyclase second
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                                                                                                                       PS00237; G PROTEIN RECEP F1 1; FAI
PS50262; G PROTEIN RECEP F1 2; 1.
n coupled receptor; Transmembrane;
1 coupled
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                     CYTOPLASMIC
2 (POTENTIA)
                                                                                                 EXTRACELLULAR
                                                                          (POTENTIAL)
                     (POTENTIAL)
                                                                                                                                                    F1_1; FALSE_NEG
F1_2; 1.
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                                               (POTENTIAL)
                                                                                               Glycoprotein. (POTENTIAL).
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SEQUENCE FROM N.A.
MEDLING=21037966; PubMed=11196645;
MEDLING=21037966; PubMed=11196645;
Hollopeter G., Jantzen H.-M., Vincent D., Li G., En
Hollopeter G., Jantzen H.-M., Nurden P., Nurden A.,

England

D.J.,

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

et ADP receptor) (P2Y(ADP)) (P2Y(cyc)) (P2T(AC))

Homo sapiens (Human) P2RY12 OR HORK3

(SP1999)

NCBI_TaxID=9606;

Conley P.B.;
"Identification of the platelet
antithrombotic drugs.";
Nature 409:202-207(2001).

targeted

SEQUENCE FROM N.A.
TISSUE-Hypothalamus;
MEDLINE=21269433; PubMed=11104774;

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CARBOHYD
CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
P2Y purinoceptor 12 (P2Y12) (P2Y12 platelet A
(ADP-glucose receptor) (ADPG-R) (P2Y(AC)) (P2
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BY SIMILARITY.

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N-LINKED (GLUNAC. . .) (POTENTI:

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6 (POTENTIAL)
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Pred. No. 6.7e-39;
1; Mismatches 101
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A KLAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A KLAUSBERG R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Whiting M., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Chan Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Chan Blakesley R.W., Touchman J.E., Jones S.J.M., Marra M.A.;

"Generation and mouse Chua semences"

"Generation and mouse Chua semences"
                                                    Zhang F.L., Luo L., G
Liu Y.-H., Chen G., P
Monama F.J. Jr.,
"ADP is the cognate 1
SP1999.",
This SWI
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-Prostate;
MEDLINE-22388257; PubMed-12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Puhl H.L. III, Ikeda S.R., Aronstam R.S.; CDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
Puhl H.L. III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of G
genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "ADP-glucose activates a G-protein coupled smooth muscle contractions."; Submitted (OCT-2000) to the EMBL/GenBank/DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmacological comparison with another
receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21394281, PubMed=11502873;
Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsum Ohishi T., Soga T., Matsushime H., Furuichi K.;
"Molecular cloning of the platelet PZT(AC) ADP receptor:
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Takeda S., Kadowaki S., Haga T., Takaesu
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                                    SIMILARITY: Belongs to
                                                  pituitary and ad the fetal brain.
SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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EMBL; AF321815; AAK00948.1; -
EMBL; AB052684; BAB60824.1; -
EMBL; AF310685; AAL32292.1; -
EMBL; AB083596; BAB89309.1; -
EMBL; AY136754; AAN01280.1; -
EMBL; BC017888; AAH17898.1; -
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Pred. No. 8.3e-39;
8; Mismatches 113;
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Bonaldo M.F., Cosavant T.L., Scheetz T.E.,

A Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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GP86_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Heart; Wang Y.-G., Gong L.; Wang Y.-G., Gong L.; "Molecular cloning of FKSG77, a novel gene encoding a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (4)
ESEQUENCE FROM N.A.
MEDLINE=22040266; PubMed=12044878;
MEDLINE=22040266; PubMed=12044878;
Mitaku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=21538899; PubMed=11546776;
Communi D., Gonzalez N.S., Detheux M., Brezillon S.,
Parmentier M., Boeynaems J.-M.;
"Identification of a novel human ADP receptor coupled
J., Biol. Chem. 276:41479-41485(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21458557; PubMed=11574155;
Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko
Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
"Discovery and mapping of ten novel G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wittenberger T., Schaller H.C., Hellebrand S.;
"An expressed sequence tag (EST) data mining strategy
the discovery of new G-protein coupled receptors.";
J. Mol. Biol. 307:799-813(2001)
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Mammalia; Eutheria;
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10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
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10-OCT-2003
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Primates;
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genes from the human
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In human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Ci. FUNCTION: Orphan receptor. Seems to be a G(i)-coupled receptor displaying a high affinity for ADP. Might play a role in hematopoiesis and the immune system.

Ci. Hematopoiesis and the immune system.

Ci. INTESUE SPECIFICITY: Strong expression in spleen and adult brain.

Ci. Lower expression in placenta, lung, liver, spinal cord, thymus, and adrenal muscle small intestine, uterus, stemach, testis, fetal brain, and adrenal gland. Not detected in pancreas, heart, kidney, skeletal muscle, ovary or fetal aorta. Clearly detected in lymph node and bone marrow, weakly detected in peripheral blood mononuclear cells (PBMC) and in peripheral blood leukocytes (PBL), but not detected in polymorphonuclear cells (PMN). In the brain, detected in all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP295368; AAK01864.1; --
EMBL; AF411113; AAL26484.1; --
EMBL; AF406692; AAL01038.1; --
EMBL; AB083597; BA889310.1; --
EMBL; AF345565; AAK29068.1; --
EMBL; BC041116; AAH41116.2; --
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GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0016526; F:G-protein coupled receptor activity, unknow.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR008109; PXYI3_purnocptor.
                                                                                                                                                                                                                                                                                                                        PRINTS; PR00237; GFCERHODOPSN.
PRINTS; PR01735; PZY13PRNCPTR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                            CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   brain regions examined.

MISCELLANBOUS: Stimulation by ADP in stably transfected CHO cells resulted in inhibition of adenylyl cyclase and the phosphorylatic of the MAP kinases MAPK3 and MAPK1 in a pertusis toxin-sensitive way. Inhibition of adenylyl cyclase and phosphorylation of the MAP kinases are transduction mechanisms that involve G(i) proteins. kinases are transduction mechanisms that involve G(i) proteins. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                           coupled
                                                          receptor;
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N-LINKED (GLCN.
N-LINKED (GLCN.
N-LINKED (GLCN.
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                        CYTOPLASMIC
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                                                                                                                                                                                                                                                                                             ransmembrane; Glycoprotein.
EXTRACELLULAR (POTENTIAL).
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Best Local Similarity
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for ADP and ATP coupled to G-protinhibit the adenylyl cyclase second messenger system
                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Frontal cortex, and Medulla oblongata;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P2YC MACFA STANDARD: PRT; 342 AA (955KG); Q95BGB; P2B-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
P2Y purinoceptor 12 (P2Y12).
                  EMBL; AB056385; BAB33041.1; -.
EMBL; AB062981; BAB60747.1; -.
InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR005394; P2Y13 purnocptor.
InterPro; IPR008109; P2Y13 purnocptor.
Pfam; PP00001; 7tm 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                      between the
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                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst Buropean Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ifted and this statement is not removed. Usage by and for contities requires a license agreement (See http://www.isb-sib.ch/ar
                                                                                                                                                                                                                                                                                                          SUBCELLULÂR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                    similarity)
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Pred. No. 1.1e-38;
7; Mismatches 96;
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AC 0358\(\textit{B}\)1;
DT 15-JUL-1998 (Rel. 36, 1)
DT 10-OCT-2003 (Rel. 42, 1)
DT 10-OCT-2003 (Rel. 42, 1)
DE UDP-glucose receptor (GN GPR105.
OS RATTUS morvegicus (Rat)
OC EUKATYOTE; Metazoa; Cho
OC Mammalia; Eutheria; Roo
OX NCBI_TAXID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97439647; PubMe
RA Charlton M.E., Williamu
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  SEQUENCE FROM N.A.
MEDLINE=97439647; PubMed=9295203;
Charlton M.E., Williams A.S., Fogliano
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(G protein-coupled receptor GPR105)
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CYTOPLASMIC (PO
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Pred. No. 2.8e-38;
9; Mismatches 114;
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N-LINKED (GLCNAC. . .) (POTENTIAL)
I -> T (IN REF. 1; BAB33041).
A -> T (IN REF. 1; BAB33041).
; E93FC26BBFF5EC4C CRC64;
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7 (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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Sciurognathi; Muridae;
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; Murinae; Rat
      P.M.,
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PRINTS; PR00237; GFCRRHODOPSN.
PRINTS; PR01655; UDPGLUCOSER.
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GO; GO:0045029; F:UDF-activated nuclectide receptor activity; ISS.
GO; GO:0007186; PG-protein coupled receptor protein signalin.
InterPro; IPR000276; GPCR khodpsn.
InterPro; IPR005466; UDPG_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http:\bar{/}/www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor regulated by immuno Brain Res. 764:141-148(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for contents and the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Receptor for UDP-glucose coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolation and characterization of a novel G protein-coupled ptor regulated by immunologic challenge.";
327
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                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                     RNTLITQQ----IIPMLYCVVFITGVLLNGISGWIFFYVPSSKSFIIYLKNIVVADFLMG
                                                                                                                                                                                                                                                                                                                       KNTTLHNEFDTIVLPVLYLIIFVASILLNGLAVWIFFHIRNKTSFIFYLKNIVVADLIMT
                             PYHVAR I PYTKSQTEGHYSCQAKETLLYTKEFTLLLSAANVCLDPI ----SISSYASRLE
                                                            PYHLCRIPFTFSHLDRLLDESAQKILYYCKBITLFLSACNVCLDPIIYFFMCRSFSRRLF 326
                                                                                                                      VNSCLFVAVLVILIGCYIAISRYIHKS---SRQFISQSSRKRKHNQSIRVVVAVFFTCFL
                                                                                                                                                                VQSVNYSKVLSVLVWVLMLLLAVPNIILTN-QSVKDVTNI-QCMELKNELGRKWHKASNY
                                                                                                                                                                                                                                LIFPFKVLSDSGLGPWQLNVFVFRVSAVIFYVNMYVSIAFFGLISFDRYYKIVKPLLVSI
                                                                                                                                                                                                                                                        LTFPFRIVHDAGFGPWYFKFILCRYTSVLFYANMYTSIVFLGLISIDRYLKVVKPFGDSR
                                                                                               VFVSIFWIVFLLLTVFYMAITRKIFKSHLKSRK--NSISVKRKSSRNIFSIVLAFVACFA
327
                                                                                                                                                                                                                                                                                                                                                                                                                                   305 AA;
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1180
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2344
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305
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47.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane;
                                                                                                                                                                                                                                                                                                                                                               Score 672.5; DB 1
Pred. No. 2.1e-37;
4; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL)

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC...)
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EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL)
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CYTOPLASMIC (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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4 (POTENTIA)
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2 (POTENTIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ransmembrane; Glycoprotein.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                   640646A68ECCC7A3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 305;
                                                                                                                                                                                                                                                                                                                                                                   88;
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                                                                                                                                                                                                                                                                                                                                                                 Indels 17;
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RC STRAIN=C55HL/GJ; TISSUE=Hippocampus, and Hypothalamus;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Puruno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Okazaki Y., Puruno M., Kasukawa T., Adachi J., Bono H., Kiyosawa H.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A.; Quackenbush J.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A.; Quackenbush J.,
RA Baldarelli R., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Balke J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Balke J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Gassterland T., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglatt D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Yaun Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Miyazaki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Mayanishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barah G.,
RA Sakai V., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RH Hayashiazki Y.,
RH Hayashiazki Y.,
RH Hayashiazki Y.,
RH Hayashiazki Y.,
RH Hayashiazki Y.,
RH Hayashiazki Y.,
RH Hayashiazki Y.,
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RH Hayashiazki Y.,
RH Hayashiazki Y.,
RH Hayashiazki Y.,
RH Hayashiazki Y.,
RH Hayashiazki Y.,
RH Hayashiazki Y.,
                            Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
                                                                                                                 Yasunishi A., Yoshino M., Waterston R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690\,(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GP86 MOUSE STANDARD;
Q9D8I2; Q8C412; Q8CAL2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21085660; PubMed=11217851;
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10-OCT-2003 (Rel. 42, Last
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Matches 127
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CONFLICT
SEQUENCE
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CARBOHYD
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein.

DOMAIN 31 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1921441; Gpr86.
InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR008109; P2Y13 purnocptor.
InterPro; IPR005466; UDPG receptor.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AK008013; BAB25409.1; -.
EMBL; AK083264; BAC38835.1; -.
EMBL; AK038560; BAC30043.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01735; P2Y13PRNCPTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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                                                                                                                                                                                    137
                       257
                                                                                                                                                122
                                                                 181
                                                                                                        197
                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                                                                                            127;
                                                                                                                                                                                                                                                                     77
                                                                                                                                                                                                                                                                                                                                                     17
                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                IDRYLKVVKPFGDSRMYSITFTKVLSVCVWVIMAVLSLPNIILTNGQPTEDNIHDCSKLK 196
                                                                                                                                                                                                                                                                                                                                    GQESHNSGNRSDGPGKNTTLHNEFDTIVLPVLYLIIFVASILLNGLAVWIFFHIRNKTSF 76
VVAVEFTCFLEYHLCRIPFTFSHLDRLLDBSAQKILYYCKEITLFLSACNVCLDFIIYFF
                                                                                                                                                                                                                                                    IFYLKNIVVADLIMTLTFPFRIVHDAGFGPWYFKFILCRYTSVLFYANMYTSIVFLGLIS 136
                                                                                                                                                                                                                                                                                                           GMQGFNKSERCPRDTRMTQL-----LFPVLYTVVFLAGILLNTVALWVFVHIPSNSTF
                                                               SPLGLWWHQVVSHTCQFIFWAVFILMLLFYAVITKKVYNSYRKFRSKDSRHKRLEVKVFI
                                                                                                        SPLGVKWHTAVTYVNSCLFVAVLVILIGCYIAISRYIHKSSRQFISQSSRKRKHNQSIRV
                                                                                                                                              FDRFLKIIMPFRKTFVKKTAFAKTVSISVWSLMFFISLPNMIL-NKEATPSSVKKCASLK
                                                                                                                                                                                                                            IVYLKNTLVADLIMALMLPFKILSDSHLAPWQLRGFVCTLSSVVFYETMYVGIMMLGLIA
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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53
61
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102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38727 MW;
                                                                                                                                                                                                                                                                                                                                                                                                             35.5%;
                                                                                                                                                                                                                                                                                                                                                                                       72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
N-LINKED (GLCNA
N-LINKED (GLCNA
N-LINKED (GLCNA
                                                                                                                                                                                                                                                                                                                                                                                          Score 666; DB 1;
Pred. No. 5.9e-37;
2; Mismatches 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F -> L (IN REF. 1).
K -> R (IN REF. 2; BAC30043).
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2 (POTENTIA:
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CYTOPLASMIC (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Frontal cortex;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M.,
Suzuki Y., Sugano S., Hashimoto K.;
TISolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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PRINTS; PR01735; P2Y13PRNCPTR.
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InterPro; IPR008109; P2Y13_purnocptor.
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InterPro; IPR000276; GPCR_Rhodpsn.
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CYTOPLASMIC ()
BY SIMILARITY
Score 491.5; DB 1;
Pred. No. 1.1e-25;
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TRANSMEM
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EMBL; AF411849; AAL47763.1; -.
GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0004930; F:G-protein coupled receptor
GO; GO:0007186; P:G-protein coupled receptor
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Joensuu T., Haemaelaeinen R., Yuan B., Johnsor Gasparini P., Zelante L., Pirvola U., Pakarine de la Chapelle A., Sankila E.-M.;
"Mutations in a novel gene with transmembrane syndrome type 3.";
"T ""Genet 68.673-684(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jacobs K.A., Collins-Racie L.A., Colbert M., Duckett M., Golden-Fleet M., Kelleher K., Kriz R., LaVallie E.R., Merberg D., Spaulding V., Stover J., Williamson M.J., McCoy J.M.; "A genetic selection for isolating cDNAs encoding secreted proteins. Gene 198:289-296(1997).
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30-MAY-2000 (Rel.
28-FEB-2003 (Rel.
                                                                          G-protein
DOMAIN
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PROSITE; PS50262; G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             syndrome type 3.";
Am. J. Hum. Genet. 69:673-684(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUB-Peripheral blood monocytes;
MEDLINE-98036061; PubMed-9370294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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Mammalia; Eutheria;
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Buropean Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in by non-profit institutions as long as its content of institutions as long as its content of institutions as long as its content of institutions as long as its content of institutions as long as its content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the second content of the seco
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SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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elaeinen R., Yuan
G_PROTEIN_RECEP_F1_1; 1.
G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane; G
EXTRACELLULAR (
1 (POTENTIAL).
48 CYTOPLASMIC (PO
48 CYTOPLASMIC (PO
69 2 (POTENTIAL).
                                                                                                  receptor;
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Primates;
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, Lehesjoki A.-E.,
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                                                                                 genomic cloning, alternative splicing, and in vitro characterization.";
J. Biol. Chem. 276:47489-47495 (2001).
J. Biol. Chem. 276:47489-47495 (2001).
J. FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. The rank order of affinities for the leukotrienes is LTC4 = LTD4 >> LTE4.
                                                                                                                                                                  Hui Y., Yang G., Galczenski H., Figueroa D.J
Copeland N.G., Gilbert D.J., Jenkins N.A., F
"The murine cysteinyl leukotriene 2 (CysLT2)
                                                                                                                                                                                                                                                                                                      Cysteinyl leukotri
CYSLTR2 OR CYSLT2.
                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
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28-FEB-2003 (Rel. 41,
28-FEB-2003 (Rel. 41,
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                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003
                                                                                                                                                                                                                      [SSUE=Heart;
                     SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Widely expressed at low levels, with highes expression in the spleen, thymus and adrenal gland, and lower i the kidney, brain and peripheral blood leukocytes.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
  SWISS-PROT
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Rodentia;
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receptor 2 (CysLTR2).
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PEAM; PFO0001; 7tm 1; 1.
PEAM; PFO0001; 7tm 1; 1.
PRINTS; PRO1533; CTSLTRECPTR.
PRINTS; PRO0237; GPCRRHODPORT,
PROSITE; PS00237; GPCRTEIN_RECEP_F1 1; FALSE_NEG.
PROSITE; PS00237; G_PROTEIN_RECEP_E1-2; 1.
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GO:0001631; F:cysteinyl leukotriene
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Pred. No. 4.5e
56; Mismatches
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PROSITE; PS00237; G_PROTEIN RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91101726; PubMed=1846231;
Honda Z.-I., Nakamura M., Miki I., Minami M., Watanabe T.
Okado H., Toh H., Ito K., Miyamoto T., Shimizu T.;
Okado H. Toh H., Ito K., Miyamoto T., Shimizu T.;
"Cloning by functional expression of platelet-activating receptor from guinea-pig lung.";
Nature 349:342-346(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae;
                                                                                               SEQUENCE
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Platelet activating factor receptor (PAF-R).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Receptor for platelet activating factor, a chemotactic phospholipid mediator that possesses potent inflammatory, smoothmuscle contractile and hypotensive activity. Seem to mediate its action via a G protein that activate a phosphatidylinositol-calcium second messenger system.

SUBCELLULAR LOCATION: Integral membrane protein.

SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                        S13638;
                        22
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4
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                     NSGNRSDGPGKNTTLHNEFDTIVLPVLYLIIFVASILLNGLAVWIFFHI---RNKTSFIF
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                                                                                                38984 MW;
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                                              74;
                                              Score 375.5; DB 1;
Pred. No. 5.7e-18;
4; Mismatches 148;
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CYTOPLASMIC (F
N-LINKED (GLCN
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5 (POTENTIAL)
CYTOPLASMIC (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
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Search o	망	8	B	8	Db	Ş	DЬ	8
Search completed: June 1, 2004, 15:17:44 Job time : 18 secs	285 NCVLDPVIYCFLTKKFRKHLSEKLNIMRSSQKCSRVTTDTGTEMAIPINHTPV 337	306 NVCLDPIIYFFMCRSFSRRLFKKSNIRTRSESIRSLQSVRRSEVRIYYDYTDV 358	226 VRRRALMMVCTVLAVFVICFVPHHMVQLPWTLAELG-MWPSSNHQAINDAHQVTLCLLST 284	247 -KRKHNQSIRVVVAVFFTCFLFYHLCRIPFTFSHLDRLLDESAQKILYYCKEITLFLSAC 305	173 CFEHYEKGSKPVLITHICIVLGFFIVFLLILFCNLVIIHTLLRQPVKQQRNAE 225	192 CSKLKSPLGVKWHTAVTYVNSCLFVAVLVILIGCYIAISRYIHKSSRQFISQSSR 246	115 RFQAVKYPIKTAQATTRKRGIALSLVIWVAIVAAASYFLVMDSTNVVSNKAGSGNITR 172	139 RYLKVVKPFGDSRMYSITFTKVLSVCVWVIMAVLSLPNIILTNGQPTEDNIHD 191

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Gapop 10.0 ,
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geneseqp2001s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Match

100.0%;

Score 1874;

DB 3;

Length 358;

Sequence 358 AA;

The present sequence is human HG03 protein, which is a G protein-coupled receptor (GPCR). It shows homology to human platelet activating factor receptor. HG03 is expressed at high levels in prostate, placenta and trachea and at low levels in thymus and testis. HG03 expression vectors can be used to transform host cells, which may be used in screening for agonists or antagonists that are potential pharmaceuticals. It can be used in gene therapy for treatment of diseases associated with low HG03 activity

Claim 1; Fig 2; 36pp; English.

694.5 37.1	696 37.1	696 37.1	700.5 37.4	700.5 37.4	40 703.5 37.5 333	735.5 39.2	742.5 39.6	742.5 39.6	762.5 40.7	768.5 41.0	768.5 41.0	768.5 41.0	768.5 41.0	768.5 41.0	768.5 41.0	768.5 41.0	768.5 41.0	
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Aaw81576	Abp70855	Aam48354	Abp70856	Aae04384	Adc55385	Aay97541	Abb80779	Aay94270	Abu63239	Ade62976	Adc33525	Adc35172	Abp81864	Abb80778	Aau84287	Aae04388	Aay58237	. 200000
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ALIGNMENTS

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                                  WPI; 2000-105698/09.
N-PSDB; AAZ29524.
Isolated human nucleic acid encoding a novel G-protein useful for the modulation, diagnosis or treatment of im
                                                                                                                    02-JUN-1998;
                                                                                                                                          02-JUN-1999;
                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                              Key
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                                                                                                                                                                                                                                                                                                                                                                     GPCR; G-protein coupled receptor; signalling pathway; drug screening assay; immune disorder; respiratory disorder; crohm's disease; multiple sclerosis; asthma; allergy; viral infection; bacterial infection; parasitic infection; cystic fibrosis; pneumonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                Human G-protein coupled 2871 receptor protein.
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                                                                                              MILLENNIUM PHARM INC
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319. .3
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/label= Extracellular_domain
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/label= Transmembrane_domain
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; Mismatches 0;
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RESULT 3
AAB83014
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XX Immu
XX Immu
XX Homo
PN JP20
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PR 23-J
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Best Local S
Matches 358
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                                                                                                                                                                                                                                             Human;
immune
                              WPI; 2001-303765/32
                                                                                           23-JUL-1999;
                                                                                                                                                      06-FEB-2001
                                                                                                                                                                                 JP2001029084-A.
                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                          Human G protein
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                                                                                                                       23-JUL-1999;
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                                                            (YAMA ) YAMANOUCHI PHARM CO LTD
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llarity 100.0%;
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                                                                                           99JP-00209919.
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                                                                                                                                                                                                                                             protein coupled receptor; antiinflammatory; inflammatory disease; bronchitis; allergy.
                                                                                                                                                                                                                                                                                          coupled receptor HORK2
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Pred. No. 6.6e-204;
; Mismatches 0;
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N-PSDB; AAF82359

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RRESULT 4
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  A new G protein coupled receptor and G protein coupled receptor gene
                                                 N-PSDB;
                                                                       WPI; 2001-321038/34
                                                                                                                                                                  17-AUG-1999;
                                                                                                                                                                                                                                                               27-FEB-2001
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                                                                                                                                                                                                                17-AUG-1999;
                                                                                                                   (YAMA ) YAMANOUCHI PHARM
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Best Local :
                                                                                                                                                                                                                                                                                                                                                       Human; G-protein coupled receptor; 2871 receptor; therapy; immune disorder; respiratory disorder; heart disorder; kidney disorder; bone marrow disorder; brain disorder; heart disorder; kidney disorder; blood vessel disorder; prostate disorder; skeletal muscle disorder; ovary disorder; epididymis disorder; spleen disorder; liver disorder; T-cells related-disorder; thymus related-disorder; breast disorder; B cells related-disorder; thyroid disorder; pancreas disorder; precursor T cell neoplasm related-disorder; antiviral; ophthalmological; antidacterial; antiallergic; antissthmatic; antirheumatic; ycostatic; antihaemorrhagic; neuroprotective; nootropic; antirheumatic; vasotropic; hepatotropic; neuroprotective; antianglnal; hypotensive; cardiant; antiarterioscleroic; nephrotropic; virualde; thrombolytic; haemostatic; antistic; haemostatic;
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Region
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                                 /label= Extracellular_domain
43. .318
/label= Transmembrane_domain
                                                                                                                                                                             Location/Qualifiers
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Pred. No. 6.6e-204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                             thyromimetic.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a human G-protein coupled receptor, 2871 receptor. The 2871 receptor is used for screening a compound that acts as agonist and antagonist to 2871 receptor. The compounds can be used for treating disorders such as immune disorders (e.g., asthma and glomerular nephritis), respiratory disorders (e.g., bronchitis and cystic fibrosis), haematopoletic disorders involving cells of leukocyte, erythroyte and platelet lineages, bone marrow disorders (e.g., leukaemias and lymphoma), brain disorders (e.g., intracranial haemorrhage, cute meningitis, multiple sclerosis and Alzheimer's disease), heart disorders (e.g., rheumatic heart disease, angina pectoris and myocardial infarction), blood vessel disorders (e.g., autosomal recessive polycystic kidney disease, acquired cystic disease and Heymann nephritis), prostate disorders (e.g., nodular hyperplasia and carcinoma), skeletal muscle disorders (e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 358 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 1A-1D; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glucksmann MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying inhibitors or modulators of novel protein, 2871 receptor, a G protein coupled receptor, useful for treating Crohn's disease, insulin dependent diabetes mellitus, multiple sclerosis, bronchial asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-DEC-1999;
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181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T-cell chronic lymphocytic leukaemia)
                          NGQPTEDNIHDCSKLKSPLGVKWHTAVTYVNSCLFVAVLVILIGCYIAISRYIHKSSRQF
                                                                                                                                                                                                                                                                           GLAVWIFFHIRNKTSFIFYLKNIVVADLIMTLTFPFRIVHDAGFGPWYFKFILCRYTSVL
                                                                                                                                                      FYANMYTSIVFLGLISIDRYLKVVKPFGDSRMYSITFTKVLSVCVWVIMAVLSLPNIILT
                                                                                                                                                                                                                                           GLAVWIFFHIRNKTSFIFYLKNIVVADLIMTLTFPFRIVHDAGFGPWYFKFILCRYTSVL
                                                                                                                                                                                                                                                                                                                                                                       MGFNLTLAKLPNNELHGQESHNSGNRSDGPGKNTTLHNEFDTIVLPVLYLIIFVASILLN
                                                                                                                                                                                                                                                                                                                                                                                                           MGFNLTLAKLPNNELHGQESHNSGNRSDGPGKNTTLHNEFDTIVLPVLYLIIFVASILLN
                                                                                                                  FYANMYTSIVFLGLISIDRYLKVVKPFGDSRMYSITFTKVLSVCVWVIMAVLSLPNIILT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-00464685
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319. .358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1874; DB 4;
Pred. No. 6.6e-204;
; Mismatches 0;
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Query Match
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Matches 358;

Similarity

100.0%; ilarity 100.0%; Conservative 0

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Mismatches

Score 1874; DB 4; Pred. No. 6.6e-204;

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358 AA;

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                                                 The present sequence represents a human octoray polypeptide. Octoray is a member of the G-protein coupled receptor family. Octoray polypeptides, polymucleotides and antibodies are useful for diagnosis and treatment of certain disease, including bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 and HIV-2, pain, cancer, diabetes, obesity, amorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders, including anxiety, schizophrenia, manic depression, depression, delirium, dementia, and severe mental retardation, dyskinesia, such as Huntington's disease or Gilles dela
                                                                                                                                                                                                                                                                                                                                                             Novel octoray polypeptides and polynucleotides encoding a G-protein coupled receptor for diagnosis and treatment of bacterial infections, cancer, neurological disorders, obesity and for identifying agonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     allergy; benign prostatic hypertrophy; migraine; vomiting; psychotic disorder; neurological disorder; anxiety; schizophrenia; manic depression; depression; delizium; dementia; mental retardation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; octoray; G-protein coupled receptor; infection; pain; cancer; diabetes; obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer;
                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-182933/18.
N-PSDB; AAF55101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bergsma DJ,
Vawter L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301
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                                                                                                                                                                                                                                                                                                         Page 27-28; 31pp;
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                                     syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence of a human octoray polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Elshourbagy NA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-US020005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease; Gilles dela tourett's syndrome.
                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guerrera SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gattu
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                                                                                                                                                                                                                                                                   Octoray is a
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03-AUG-2001;
08-NOV-2001;
13-NOV-2001;
12-APR-2002;
The present invention describes a method for detecting a bladder cancer-
associated transcript in a cell from a patient. The method comprises
contacting a biological sample from the patient with a polynucleotide
that selectively hybridises to a sequence that is 80 % identical to a
table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
encode the human bladder cancer-associated proteins given in ABR48146 to
ABR48242). Bladder cancer-associated sequences from the present invention
have cytostatic activities, and can be used in antisense gene therapy and
                                                                                                                                                     Detecting a bladder cancer-associated transcript in a cell patient, comprises contacting a biological sample from the bladder cancer-associated polynucleotide or antibody.
                                                                                                                           Claim 10; Page 277; 307pp; English.
                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                               03-JUL-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; bladder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human bladder cancer associated protein sequence SEQ ID NO:135
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Best Local Similarity
                                                                                 18-APR-2001;
10-MAY-2001;
09-NOV-2001;
13-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in vaccine production. The method can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in various screening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications
                                                                                                                                                                                                                                                                Lung cancer-associated polypeptide; cytostatic; emphysema; antiinflammatoxy; antiasthmatic; non-small cell lung cancer; atelect. small cell lung cancer; benign lesion; precancerous lesion; bronchit chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                                                       29-NOV-2001;
12-APR-2002;
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                                                     ; 2001US-0284770P.
; 2001US-0290492P.
; 2001US-0339245P.
; 2001US-0350666P.
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; 2002US-0372246P.
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Pred. No. 6.6e-204;
); Mismatches 0;
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                                   Human cancer-related protein,
                                                                          19-MAY-2003
                                                                                                               ABR01795
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Pred. No. 6.6e-204;
; Mismatches 0;
                                     154P2A8
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Human;

cytostatic; vaccine; cancer; immune response.

RESULT 10 ABP81966 ID ABP81

ABP81966

standard; protein; 358

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Best Local
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10-APR-2001;
25-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                    FYANMYTSIVELGLISIDRYLKVVKPFGDSRMYSITFTKVLSVCVWVIMAVLSLENIILT
                                                                                                                              NGQPTEDNIHDCSKLKSPLGVKWHTAVTYVNSCLFVAVLVILIGCYIAISRYIHKSSRQF
                                                                                                                                                                                                                                              GLAVWIFFHIRNKTSFIFYLKNIVVADLIMTLTFPFRIVHDAGFGPWYFKFILCRYTSVL 120
              FLSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTRSESIRSLQSVRRSEVRIYYDYTDV
                                                                                                                                                                                                                            GLAVWIFFHIRNKTSFIFYLKNIVVADLIMTLTFPFRIVHDAGFGPWYFKFILCRYTSVL
                                                                                                                                                                                                                                                                                                                                                                                                 358
                                                                       ISQSSRKRKHNQSIRVVVAVFFTCFLPYHLCRIPFTFSHLDRLLDESAQKILYYCKEITL
                                                                                                             NGQPTEDNIHDCSKLKSPLGVKWHTAVTYVNSCLFVAVLVILIGCYIAISRYIHKSSRQF
                                                                                                                                                                      FYANMYTSIVFLGLISIDRYLKVVKPFGDSRMYSITFTKVLSVCVWVIMAVLSLPNIILT
                                                      ISQSSRKRKHNQSIRVVVAVFFTCFLPYHLCRIPFTFSHLDRLLDESAQKILYYCKEITL
                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1874; DB 6; llarity 100.0%; Pred. No. 6.6e-204; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001US-0282739P.
2001US-0283112P.
2001US-0286630P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raitano
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Human G 04-MAR-2003 ABP81966;

(first entry)

protein-coupled receptor GPR87/95 protein SEQ ID NO:418.

당 - 성

120

60

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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino CC acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; CC and (2) an isolated antibody having high specificity and high affinity or CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in CC gene therapy. The antigenic peptides for GPCRs are useful in detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs are useful for detecting the CC presence or absence of corresponding GPCRs. The antigenic peptides for CPCRs and antibodies are also useful for detecting the reating immune-related diseases, growth-related diseases, cell CC regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, cell cc atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoparthritis, osteoparosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, disease, disease, disease, disease, parkinson's disease, multiple sclerosis, pain, psoriasis, cancer, cardiomyopathy, chronic and acute disease, paintery, depression, schizophrenia, descrosis, obesity, nausea, hypertension, comportension, renal disorders, rheumatoid arthritis, trauma, ulcers, or canny other disease and immunodisgonesis. NaEA4523 to ABZ4369 encode CC GPCR proteins given in ABP81675 to ABP82018, which are used in the cc gPCR proteins of the present invention
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1; 523pp; English.
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100.0%;
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Score 1874; DB 6;
Pred. No. 6.6e-204;
                 Length 358;
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RESULT 11
ABU09897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KW Human; receptor; G-protein coupled receptor; gene therapy; pneumonia;
xw immune disorder; Crohn's disease; Grave's disease; respiratory disorder;
xw diphtheria; haematopoietic disorder; leukaemia; systemic sclerosis;
xw prostatic disorder; benign prostate hypertrophy; tumour; breast disease;
xw acute mastitis; Paget's disease; muscular disease; rhabdomyosarcoma;
xw neurological disorder; cerebral oedema; Parkinson's disease; atrophy;
xw blood vessel disorder; atherosclerosis; testicular disease; syphilis;
xw epididymal disease; thyroid disease; hyperthyroidism; cretinism; AIDS;
xw epididymal disease; thyroid disease; hyperthyroidism; cretinism; AIDS;
xw epididymal disease; part failure; pericarditis; pancreatic disease;
xw pancreatitis; diabetes mellitus; thymus disease; thymic hypoplasia;
xw pancreatitis; diabetes mellitus; thymus disease; thymic hypoplasia;
xw Hodgkin disease; spleen disease; splenomegaly; Gaucher disease;
xw Hodgkin disease; splenomegaly; Gaucher disease;
xw Hodgkin disease; splenomegaly; Gaucher disease;
xw Hodgkin disease; splenomegaly; Gaucher disease;
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                                                                                                             02-JUN-1998;
02-SEP-1998;
21-JAN-1999;
02-JUN-1999;
28-JUN-1999;
26-AUG-1999;
16-DEC-1999;
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MILLENNIUM PHARM INC
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98US-00145745.
99US-00234923.
99US-00324465.
99US-00340880.
99US-00383745.
99US-00464685.
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밁 S 밁 á 밁 ð 밁 S 밁 Ş

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The invention relates to an isolated G-protein coupled receptor nucleic cc acid molecule encoding the G-protein coupled receptors 2871, 14926, 17723 cc and 23992. The nucleic acid molecule is useful in monitoring, diagnosing cd and treating immune disorders (e.g. Crohn's disease and Graw's disease); cc disorders (e.g. leukaemia and systemic sclerosis); haematopoietic cc disorders (e.g. penumonia or diphtheria); haematopoietic cc quite mastitis and paget's disease); muscular disorders (e.g. cc acute mastitis and paget's disease); muscular disorders (e.g. cc rhabdomyosarcoma); neurological disorders (e.g. ccrebral oedema and cc rharosclerosis); diseases involving testis and epiddymis (e.g. atrophy cc atherosclerosis); diseases involving testis and epiddymis (e.g. atrophy cc and syphilis); thyroid diseases (e.g. hyperthyroidiam and cretinism); cc and syphilis); thyroid diseases (e.g. hyperthyroidiam and cretinism); cc diseases (e.g. pancreatitis and diabetes mellitus); diseases involving cc diseases (e.g. pancreatitis and diabetes mellitus); diseases involving cc diseases (e.g. pancreatitis and diabetes mellitus); diseases involving cc diseases (e.g. pancreatitis and diabetes mellitus); diseases involving the spleen (e.g. splenomegaly and Gaucher disease); diseases (e.g. involving the liver (e.g. hepatic failure and alcoholic liver disease); cell disorders (e.g. systemic lupus erythematosus and AIDS); B-cell coll disorder (e.g. systemic lupus erythematosus and AIDS); B-cell (e.g. thrombocytopenia and haemolytic-uraemic syndrome). The nucleic (e.g. thrombocytopenia and haemolytic-uraemic syndrome). The nucleic coll present sequence represents the amino acid sequence of the human G-creation councied receptor 2871
RESULT 12
AAE34531
ID AAE34
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Matches 358
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                                                                                                              ISQSSRKRKHNQSIRVVVAVFFTCFLFYHLCRIPFTFSHLDRLLDESAQKILYYCKEITL
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I, Weich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel Mowgli G-protein coupled receptor (GPCR) polypeptides and polynucleotides. Mowgli polypeptides, nucleic acids, probes, antibodies, expression vectors and ligands are useful as the probes, antibodies, expression vectors and ligands are useful as with over-, under- or abnormal expression of Mowgli GPCR in tissues, in with over-, under- or abnormal expression of Mowgli GPCR in tissues, in with over-, under- or abnormal expression of Mowgli GPCR in tissues, in with over-, under- or abnormal expression of Howgli Polypeptides of the genetic analysis and in chromosome identification. Polypeptides of the invention may be used for screening compounds which bind the receptor and invention and year of the produce antibody and/or T cell immune response against e.g. bacterial, produce antibody and/or T cell immune response against e.g. bacterial, protozoan, fungal or viral infections, pain, cancers, diabetes, obesity, protozoan, sethma, Parkinson's disease and other neurological disorders. anorexia, asthma, Parkinson's disease and other neurological disorders.
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N-PSDB; AAD52809.
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18-MAY-2001; 2001US-0292141P:
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 358; Conservative 0
                                                                                                                                                                                 The invention relates to novel Mowgli G-protein coupled receptor (GPCR) polypeptides and polynucleotides. Mowgli polypeptides, nucleic acids, probes, antibodies, expression vectors and ligands are useful as biosensors, for detection, diagnosis, or treatment of diseases associated with over-, under- or abnormal expression of Mowgli GPCR in tissues, in genetic analysis and in chromosome identification. Polypeptides of the invention may be used for screening compounds which bind the receptor and which activate (agonists) or inhibit (antagonist) activation of Mowgli. They may further be used as vaccines to induce immunological response to produce antibody and/or T cell immune pain, cancers, diabetes, obseity, anorexia, asthma, Parkinson's disease and other neurological disorders. The present sequence is human Mowgli G-protein coupled receptor with FLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Mowgli G-protein coupled receptor polypeptides and polynucleotides, useful for inducing immunological response to produce antibody and/or T cell immune response against e.g. bacterial, fungal, protozoan or viral
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Region
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                                                                                                            Sequence
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18-MAY-2001;
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2001US-0292141F.
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Mismatches 0;
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Region
                                                                                          New Mowgli G-protein coupled receptor polypeptides and polynucleotides, useful for inducing immunological response to produce antibody and/or T cell immune response against e.g. bacterial, fungal, protozoan or viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mowgli G-protein coupled receptor; GPCR; immune response; in: neurological disorder; Parkinson's disease; obesity; asthma; anorexia; pain; diabetes; vaccine; human.
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CC polypeptides and polynucleotides. Mowgli polypeptides, nucleic acids,
CC probes, antibodies, expression vectors and ligands are useful as
CC probes, antibodies, expression vectors and ligands are useful as
CC biosensors for detection, diagnosis, or treatment of diseases associated
CC with over-, under- or abnormal expression of Mowgli GPCR in tissues, in
CC genetic analysis and in chromosome identification. Polypeptides of the
CC invention may be used for screening compounds which bind the receptor and
CC which activate (agonists) or inhibit (antagonist) activation of Mowgli,
CC which activate (agonists) or inhibit (antagonist) activation of Mowgli,
CC protozoan, fungal or vised as vaccines to induce immunological response to
CC protozoan, fungal or viral infections, pain, cancers diabetes, obesity,
CC protozoan, sethma, Parkinson's disease and other neurological disorders.
CC and vice tar
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29-JUL-1999; 99JP-00248036.
27-AUG-1999; 99JP-00300253.
27-BOCT-1999; 99US-0159590P.
11-JAN-2000; 2000JP-00118776.
17-FEB-2000; 2000US-0183322P.
02-MAY-2000; 2000UP-00183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                              C-PLACE1003238; guanosine triphosphate binding protein coupled receptor; cytostatic; nootropic; neuroprotective; brain disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human C-PLACE1003238 protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New gene encoding guanosine triphosphate binding protein coupled receptor, and the protein and antibodies to it, for diagnosing ar treating disease such as brain disease.
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N-PSDB; AAH47235.
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